

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 24, 2004, 00:54:41 ; Search time 76 Seconds

(without alignments)
2245,509 Million cell updates/sec

Title: US-08-064-271-10

Sequence: 1 MABALLICVALSHSTAMP.....RSGLDINPTLKERSTEL 604

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Geneseqp29yand04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3237	100.0	604	2	Aat56660 Cyclooxyc
2	3237	100.0	604	2	Aat72228 Human cyc
3	3237	100.0	604	4	Aab72199 Human pro
4	3237	100.0	604	5	Abp65138 Hypoxia-r
5	3237	100.0	604	5	Abb07244 Human cyc
6	3237	100.0	604	6	ABU03521 Angiogene
7	3237	100.0	604	6	ABR42250 Human cyc
8	3237	100.0	604	7	ADA20299 Human cyc
9	3237	100.0	604	7	ABM78951 Breast ca
10	3237	100.0	604	7	ADD27955 Human COX
11	3234	99.9	604	7	AAW12698 Human pro
12	3140	97.0	604	2	AAR51267 Sequence
13	2992	92.4	604	5	ABR07248 Human pro
14	2971	91.8	604	5	ABR07248 Human pro
15	2971	91.7	604	5	ABR07242 Rabbit cy
16	2967	91.7	604	5	ABG30577 Dog prost
17	2967	91.7	604	5	ABG30577 Dog prost
18	2967	91.7	604	5	ABD27957 Canine cy
19	2938	90.8	604	5	ABD27957 Canine cy
20	2938	90.8	604	5	ABD27959 Horse cyc
21	2932	90.3	604	7	ABD27958 Equine CO
22	2892	89.3	604	5	ABR07247 Guinea pi
23	2891	89.3	604	5	ABR07250 Sheep cyc
24	2891	89.3	604	7	ADD27961 Guinea pi
25	2881.5	89.0	603	7	ADD27956 Ovine COX

26	2877	88.9	604	7	ADD27962 Murine CO
27	2873	88.8	604	2	Aaw12699 Mouse pro
28	2873	88.8	604	5	ABBS7358 Mouse isc
29	2868	88.6	604	5	ABR07245 Mouse cyc
30	2868	88.6	604	6	ABR42252 Mouse cyc
31	2865	88.5	604	2	AAR51268 Sequence
32	2862	88.4	604	5	ABR07246 Rat cyclo
33	2834	87.6	604	7	ADD27964 Mink COX-
34	2818	87.1	604	7	ADD27963 Rat COX-
35	2741	84.7	582	7	ADD27945 COX-2 ami
36	2734	84.5	604	5	ABR07251 Chicken c
37	2725.5	84.2	581	7	ADD27965 COX-2 ami
38	2718.5	84.0	603	7	ADD27965 Chicken C
39	2434	75.2	607	7	ADD27967 Brook tro
40	2417	74.7	607	7	ADD27967 Rainbow t
41	2037.5	62.9	606	7	ADD27939 Rabbit CO
42	2037	62.9	599	5	ABG96403 Human ova
43	2037	62.9	599	6	ABR42249 Human cyc
44	2037	62.9	599	7	ADC24199 Human NOV
45	2037	62.9	599	7	ADD27936 Human COX

ALIGNMENTS

RESULT 1

ID AAR56660 standard; protein; 604 AA.

AC	XX	AAR56660;	
DT	XX	25-MAR-2003 (revised)	
DT	XX	27-FEB-1995 (first entry)	
DE	XX	Cyclooxxygenase-2.	
DE	XX	Cyclooxxygenase-2.	
KW	XX	Cyclooxxygenase-2; enzyme; osteosarcoma; antiinflammatory; assay.	
OS	XX	Homo sapiens.	
PN	XX	WO9414977-A1.	
PD	XX	07-JUL-1994.	
PF	XX	17-DEC-1993; 93WO-CA000547.	
PR	XX	22-DEC-1992; 92US-00994760.	
PR	XX	06-MAY-1993; 93US-00064271.	
PA	XX	(MERI) MERCK FROST CANADA INC.	
PI	XX	Cromlish WA, Kennedy BP, Oneill G, Vickers PJ, Wong E;	
PI	XX	Manclini JA;	
XX	XX	WPI; 1994-263635/32.	
DR	XX	N-PSDB; AAQ71002.	
PT	XX	Assays for cyclo:oxxygenase-1 and -2 - for identifying selective	
PT	XX	antagonists, i.e. potential anti inflammatory etc., also new human	
PT	XX	cyclo:oxxygenase-2 and cDNA encoding it.	
PS	XX	Disclosure; Fig 1A-1C; 55pp; English.	
CC	XX	The human cyclooxxygenase-2 COX-2 protein is used in assays to identify	
CC	XX	inhibitors, which have antiinflammatory, analgesic, antipyretic and	
CC	XX	anticancer activity. (Updated on 25-MAR-2003 to correct PN field.)	
SQ	XX	Sequence 604 AA:	

Query Match 100.0%; Score 3237; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.6e-300;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MLARALLICAVIALSHTANPCCSHPCCNRGYCMVGDFQYKDCCTRTGFGYGENCSTPEFL 60
DB 1 MLARALLICAVIALSHTANPCCSHPCCNRGYCMVGDFQYKDCCTRTGFGYGENCSTPEFL 60
QY 61 TRIKLFKPTPTVTHYILTHFKGFNNVNNIPFLNAINMSYVLTSSRLIDSPPTYNADY 120
DB 61 TRIKLFKPTPTVTHYILTHFKGFNNVNNIPFLNAINMSYVLTSSRLIDSPPTYNADY 120
QY 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIIDPQGS 180
DB 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIIDPQGS 180
QY 181 NMFAFAFHQFTHQFCKTDHKGPAFTNGLGHVLDNHIYGETLARQRKRLFKDGKMKY 240
DB 181 NMFAFAFHQFTHQFCKTDHKGPAFTNGLGHVLDNHIYGETLARQRKRLFKDGKMKY 240
QY 241 QIIDGEMYPPTVKDQAEIYPPQVEHLRFVAGGVFGVGLVGLMMYATITWLREHNRVCD 300
DB 241 QIIDGEMYPPTVKDQAEIYPPQVEHLRFVAGGVFGVGLVGLMMYATITWLREHNRVCD 300
QY 301 VLKQEHPEWGDQQLFQTSRLILIGETIKIVIEDYVQHLGSGYHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQEHPEWGDQQLFQTSRLILIGETIKIVIEDYVQHLGSGYHFKLKPDELLFNKQFOYQ 360
QY 361 NR1AAEFNTLYHMHPLPPTFOIHDOKYNYQOPIYNNLSILHEGITOQVSESTFQIAGRV 420
DB 361 NR1AAEFNTLYHMHPLPPTFOIHDOKYNYQOPIYNNLSILHEGITOQVSESTFQIAGRV 420
QY 421 AGGRNVPVAVQKVSASIDQSRQMKYQSFNEYRKRFLKPYESFEEITGKEMSALELAL 480
DB 421 AGGRNVPVAVQKVSASIDQSRQMKYQSFNEYRKRFLKPYESFEEITGKEMSALELAL 480
QY 481 YGDIIDAVELYPALVVEKPRPDALFGETMVEVGAFFSLKGLMGVNICSPAYWKPTGGEV 540
DB 481 YGDIIDAVELYPALVVEKPRPDALFGETMVEVGAFFSLKGLMGVNICSPAYWKPTGGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPPELIKTVTINASSRSGLDINPTVLKER 600
DB 541 GFOIINTASIOSLICNNVKGCPFTSFVDPPELIKTVTINASSRSGLDINPTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

RESULT 2
ID AAR72228 standard; protein: 604 AA.
XX
AC AAR72228;
XX
DT 25-MAR-2003 (revised)
DT 28-SEP-1995 (first entry)
XX
DE Human cyclooxygenase-2.
XX
KW Cyclooxygenase-2; COX-2; COX-1; inhibitor; screening; osteosarcoma.
XX
OS Homo sapiens.
XX
PN W09509238-A1.
XX
PD 06-APR-1995.
XX
PE 13-SEP-1994; 94WO-CA000501.
XX
PR 27-SEP-1993; 93US-00084033.
XX
PA (MERI ) MERCK FROST CANADA INC.
XX
PI Oneil GP, Mancini JA;
XX
DR WPI, 1995-147436/19.

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DR N-PSDB; AA089376.
XX High level expression of human cyclooxygenase (COX)-2 - using new 3'
PT flanking region from COX-1, useful in assays for identifying potent,
PT selective or preferential inhibitors of COX-2.
XX Disclosure; Fig 1; 59pp; English.
XX
CC Full-length cDNA derived from human osteosarcoma cells (given in
CC AA089376) encoded human COX-2 (AAR72228). High-level expression of COX-2
CC in COS7 cells was achieved using a vaccinia or baculovirus vector and a
CC construct in which COX-2 cDNA was attached at its 5' end to a 3' flanking
CC sequence of human COX-1 cDNA (AA089377). (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 604 AA;
Query Match 100.0%; Score 3237; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 1,66-300;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLARALLICAVIALSHTANPCCSHPCCNRGYCMVGDFQYKDCCTRTGFGYGENCSTPEFL 60
DB 1 MLARALLICAVIALSHTANPCCSHPCCNRGYCMVGDFQYKDCCTRTGFGYGENCSTPEFL 60
QY 61 TRIKLFKPTPTVTHYILTHFKGFNNVNNIPFLNAINMSYVLTSSRLIDSPPTYNADY 120
DB 61 TRIKLFKPTPTVTHYILTHFKGFNNVNNIPFLNAINMSYVLTSSRLIDSPPTYNADY 120
QY 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIIDPQGS 180
DB 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIIDPQGS 180
QY 181 NMFAFAFHQFTHQFCKTDHKGPAFTNGLGHVLDNHIYGETLARQRKRLFKDGKMKY 240
DB 181 NMFAFAFHQFTHQFCKTDHKGPAFTNGLGHVLDNHIYGETLARQRKRLFKDGKMKY 240
QY 241 QIIDGEMYPPTVKDQAEIYPPQVEHLRFVAGGVFGVGLVGLMMYATITWLREHNRVCD 300
DB 241 QIIDGEMYPPTVKDQAEIYPPQVEHLRFVAGGVFGVGLVGLMMYATITWLREHNRVCD 300
QY 301 VLKQEHPEWGDQQLFQTSRLILIGETIKIVIEDYVQHLGSGYHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQEHPEWGDQQLFQTSRLILIGETIKIVIEDYVQHLGSGYHFKLKPDELLFNKQFOYQ 360
QY 361 NR1AAEFNTLYHMHPLPPTFOIHDOKYNYQOPIYNNLSILHEGITOQVSESTFQIAGRV 420
DB 361 NR1AAEFNTLYHMHPLPPTFOIHDOKYNYQOPIYNNLSILHEGITOQVSESTFQIAGRV 420
QY 421 AGGRNVPVAVQKVSASIDQSRQMKYQSFNEYRKRFLKPYESFEEITGKEMSALELAL 480
DB 421 AGGRNVPVAVQKVSASIDQSRQMKYQSFNEYRKRFLKPYESFEEITGKEMSALELAL 480
QY 481 YGDIIDAVELYPALVVEKPRPDALFGETMVEVGAFFSLKGLMGVNICSPAYWKPTGGEV 540
DB 481 YGDIIDAVELYPALVVEKPRPDALFGETMVEVGAFFSLKGLMGVNICSPAYWKPTGGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPPELIKTVTINASSRSGLDINPTVLKER 600
DB 541 GFOIINTASIOSLICNNVKGCPFTSFVDPPELIKTVTINASSRSGLDINPTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

RESULT 3
ID AAB72199 standard; protein: 604 AA.
XX
AC AAB72199;
XX
DT 02-MAY-2001 (first entry)

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XX DE Human prostaglandin-endoperoxide synthase 2 (PTGS2) protein.
 XX KW Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
 KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
 KW inflammation.
 XX OS Homo sapiens.
 XX FT Key location/Qualifiers
 FT Misc-difference 587 /note="Optionally Arg when variation occurs in DNA
 FT sequence due to single nucleotide polymorphism"
 XX MO200107662-A1.
 XX PD 01-FEB-2001.
 XX PF 24-JUL-2000; 2000WO-US020114.
 XX PR 22-JUL-1999; 99US-0145170P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;
 XX DR WPI; 2001-182805/18.
 XX N-RSDB; AAF80896, AAF80897.
 XX PT New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
 PT for gene therapy of inflammation and for establishing a genotype or
 PT haplotype.
 XX PS Claim 10; Fig 3; 118bp; English.
 XX CC This invention relates to a polynucleotide sequence that is a polymorphic
 CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
 CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
 CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
 CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
 CC protein is represented by AAF872199. The invention includes PCR and
 CC sequencing primers, and probes represented in AAF80898 - AAF81151 which
 CC are used to isolate and characterize the PTGS2 gene sequence, and to
 CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide
 CC sequences are used to express variant PTGS2 proteins, for structural
 CC analysis or drug-binding studies and also in gene therapy (either
 CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
 CC useful for diagnosis, prognosis and therapy and analysis of the new, and
 CC known, polymorphisms and used to determine PTGS2 haplotype and genotype,
 CC especially for determining association between a particular trait, e.g. a
 CC clinical response to drugs that target PTGS2 but also disease
 CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
 CC used for developing diagnostic tests and treatments for immune-related
 CC disorders such as arthritis and inflammation. The polymorphisms may also
 CC be used to study expression and biological function of PTGS2. Transgenic
 CC animals that express PTGS2 are used to study expression of PTGS2
 CC isogenes, for in vivo drug screening and testing, and for assessing
 CC effects of therapeutic agents
 XX SQ Sequence 604 AA;
 XX
 XX Query Match 100.0%; Score 3237; DB 4; Length 604;
 XX Best Local Similarity 100.0%; Pred. No. 1.6e-300;
 XX Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 MLARALLICAVLAISHTANPCSCSHPCQNRGVCMSGVGYQYKDCDRTGFGYGENCSTPEFL 60
 XX DB 1 MLARALLICAVLAISHTANPCSCSHPCQNRGVCMSGVGYQYKDCDRTGFGYGENCSTPEFL 60
 XX QY 61 TRILFLKPTNTYVHYILTHKGFNNVNNIPLRLNALMSYVLTSSHLIDSPPTYNADY 120
 XX DB 61 TRILFLKPTNTYVHYILTHKGFNNVNNIPLRLNALMSYVLTSSHLIDSPPTYNADY 120
 XX DR 61 TRILFLKPTNTYVHYILTHKGFNNVNNIPLRLNALMSYVLTSSHLIDSPPTYNADY 120

QY 121 GYKSEAFSNLSYTRALPVVDDCPPTPLGVKQKQLPDSNEIYKLLRRKKFIPDPGGS 180
 DB 121 GYKSEAFSNLSYTRALPVVDDCPPTPLGVKQKQLPDSNEIYKLLRRKKFIPDPGGS 180
 QY 181 NMMEFAPPAOHTHOFFYTDHKKRGPATNGLGCHGVDLNHYIYETLAROKRLFPDQKMKY 240
 DB 181 NMMEFAPPAOHTHOFFYTDHKKRGPATNGLGCHGVDLNHYIYETLAROKRLFPDQKMKY 240
 QY 241 QIIDGEMYPPTVKTOEMMYPPPOVPEHLRPAVQGEVGLVGLMMYATILREHNRVCD 300
 DB 241 QIIDGEMYPPTVKTOEMMYPPPOVPEHLRPAVQGEVGLVGLMMYATILREHNRVCD 300
 QY 301 VLKQHEPMEGDEQLFQTSRLILGETTKIYIEDVQHLSCGHFLKATKDPPELLFNKQFOYQ 360
 DB 301 VLKQHEPMEGDEQLFQTSRLILGETTKIYIEDVQHLSCGHFLKATKDPPELLFNKQFOYQ 360
 QY 361 NR1AAEFNTLYHMHPLLPDTFQIHDQKYNQOFTYNNSSILLEGITQFVSEFTQIAGR 420
 DB 361 NR1AAEFNTLYHMHPLLPDTFQIHDQKYNQOFTYNNSSILLEGITQFVSEFTQIAGR 420
 QY 421 AGGRNVPVAVQXYSQASIDQSRQMKYQSENEYKRRFMLKPYSEFEBLTGKEMSALEAL 480
 DB 421 AGGRNVPVAVQXYSQASIDQSRQMKYQSENEYKRRFMLKPYSEFEBLTGKEMSALEAL 480
 QY 481 YGDIIDAVELYPALVKEKPRPDATFGETMVEVGAPEFLKGLMGVATGSPAWKSTTGEV 540
 DB 481 YGDIIDAVELYPALVKEKPRPDATFGETMVEVGAPEFLKGLMGVATGSPAWKSTTGEV 540
 QY 541 GFQIINTVASTIQLICNNVKGCPPTSFVDPDELIKTYTINASSRSGLDINFTVILKER 600
 DB 541 GFQIINTVASTIQLICNNVKGCPPTSFVDPDELIKTYTINASSRSGLDINFTVILKER 600
 QY 601 STEL 604
 DB 601 STEL 604
 XX
 XX RESULT 4
 XX ABBP65138
 XX ID ABBP65138 standard; protein; 604 AA.
 XX AC ABBP65138;
 XX DT 12-NOV-2002 (first entry)
 XX DE Hypoxia-regulated protein #12.
 XX XX Cytostatic; vasotropic; tranquilizer; antiatherosclerotic; gene therapy;
 KW antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine;
 KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
 KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
 KW preclampsia; atherosclerosis; inflammatory condition; wound healing;
 KW inflammation; erythropoiesis; hair loss; human.
 XX OS Homo sapiens.
 XX FT Key location/Qualifiers
 FT Misc-difference 587 /note="Optionally Arg when variation occurs in DNA
 FT sequence due to single nucleotide polymorphism"
 XX MO200246465-A2.
 XX PD 13-JUN-2002.
 XX PF 10-DEC-2001; 2001WO-GB005458.
 XX PR 08-DEC-2000; 2000GB-00030076.
 XX PR 08-FEB-2001; 2001GB-00003156.
 XX PR 25-OCT-2001; 2001GB-00025666.
 XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
 XX Rayner MN;
 XX WPI; 2002-627238/67.

Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell types under different conditions and identifying a differentially regulated gene.

Claim 35, Page 338-339, 538bp, English.

The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV7873-ABV7816 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumorigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss

Sequence 604 AA:

Query Match 100.0%; Score 3237; DB 5; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.6e-300;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLARALLICAVIALSHTANPCSHPCNRCVCMVSGFDQKCDCTRTGFGENCSTPEFL 60
1 MLARALLICAVIALSHTANPCSHPCNRCVCMVSGFDQKCDCTRTGFGENCSTPEFL 60
61 TRIKFLKPTNTVHYLLTHRGKFWNVNVPFLNATMSYVLTSRSHLIDSPPTYNADY 120
61 TRIKFLKPTNTVHYLLTHRGKFWNVNVPFLNATMSYVLTSRSHLIDSPPTYNADY 120
121 GYKSWENAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIIDPQGS 180
121 GYKSWENAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIIDPQGS 180
121 GYKSWENAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIIDPQGS 180
181 NMWFAFAQHFTTHQFPTDHRKGAFTNGCHGVLDNHIYETLARQKRLTFDQGMKY 240
181 NMWFAFAQHFTTHQFPTDHRKGAFTNGCHGVLDNHIYETLARQKRLTFDQGMKY 240
241 QIIDGEMWPTVKTQEMTIPPOVPEHRAVGOEYFGLVPGMMATIMLRSHNVCD 300
241 QIIDGEMWPTVKTQEMTIPPOVPEHRAVGOEYFGLVPGMMATIMLRSHNVCD 300
301 VLKQEHMEWGDEQLFQTSRLILIGETIKIVIEDYVOHLGSYHFKLKPDELLFNKKQFOYQ 360
301 VLKQEHMEWGDEQLFQTSRLILIGETIKIVIEDYVOHLGSYHFKLKPDELLFNKKQFOYQ 360
361 NRIAAEFTLYHMFLLPDTFOIHQKNYQOFTYNNLSLLEHGTQVSEFTROIAGRV 420
361 NRIAAEFTLYHMFLLPDTFOIHQKNYQOFTYNNLSLLEHGTQVSEFTROIAGRV 420
421 AGGRVPRPAVOKVASIDQSRQMKYQSFNEKRKPFMLKPYSPFELLGKEMSALEBAL 480
421 AGGRVPRPAVOKVASIDQSRQMKYQSFNEKRKPFMLKPYSPFELLGKEMSALEBAL 480
481 YGDIIDAVELYPALVEKERPDALFGETWVEVGAFFSLKGLMGNTVCSAPYWKSPSTFGEV 540
481 YGDIIDAVELYPALVEKERPDALFGETWVEVGAFFSLKGLMGNTVCSAPYWKSPSTFGEV 540
541 GFQIINTASIOSLLNNNKGCPFTSFVPDELLITVTNTINASSSGGDDINPTVLKER 600
541 GFQIINTASIOSLLNNNKGCPFTSFVPDELLITVTNTINASSSGGDDINPTVLKER 600
601 STEL 604

DB 601 STEL 604

RESULT 5
AB07244
ID ABB07244 standard; protein; 604 AA.

AC ABB07244;
XX
XX 26-MAR-2002 (first entry)
XX
XX

DE Human cyclooxygenase-2 (COX-2) protein.

KW Cyclooxygenase; COX-1; COX-2; canine; arthritis; cancer; neoplasia;
XX inflammation; central nervous system; human.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Misc-difference 165
FT /note="encoded by GGA"

PN WO200111026-A1.

PD 15-FEB-2001.

PF 04-AUG-2000; 2000MO-US019565.

PR 06-AUG-1999; 99US-0147601P.

PA (SEAR) SEARLE & CO G D.

PI Gliese JK;

XX MPI; 2002-113777/15.

XX N-PSDB; ABB94344.

PT Novel substantially purified canine cyclooxygenase 1 or 2 protein, useful for identifying drugs that can reduce inflammation in dogs, and screening selective inhibitors of cyclooxygenase-2 protein.

PS Disclosure; Page 97-99; 122pp; English.

XX The invention relates to genes that encode canine cyclooxygenase (COX)-1 or COX-2 proteins. The COX proteins, especially COX-2 is useful for its diagnosing or prognosing a COX-2 related condition in a dog. COX-2 or its fragment is useful for identifying a test material which has the ability to inhibit, suppress, modulate, or maintain canine COX-2 activity. The COX-1 and COX-2 polynucleotides are useful for determining an association between a polymorphism and a trait. COX-2 cDNA molecules and methods provided are also useful for diagnosing or prognosing COX-2 related condition such as arthritis, cancer, neoplasia, inflammation or central nervous system disorder in a dog. The present sequence represents a human COX-2 protein

Sequence 604 AA:

Query Match 100.0%; Score 3237; DB 5; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.6e-300;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLARALLICAVIALSHTANPCSHPCNRCVCMVSGFDQKCDCTRTGFGENCSTPEFL 60
1 MLARALLICAVIALSHTANPCSHPCNRCVCMVSGFDQKCDCTRTGFGENCSTPEFL 60
61 TRIKFLKPTNTVHYLLTHRGKFWNVNVPFLNATMSYVLTSRSHLIDSPPTYNADY 120
61 TRIKFLKPTNTVHYLLTHRGKFWNVNVPFLNATMSYVLTSRSHLIDSPPTYNADY 120
121 GYKSWENAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIIDPQGS 180
121 GYKSWENAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIIDPQGS 180
121 GYKSWENAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIIDPQGS 180

QY 181 NMFAFFAOFHTHOFKTDHKGPAFTNGIGHGVLDNHIYGETLAROKRLRFKDGKMKY 240
 DB 181 NMFAFFAOFHTHOFKTDHKGPAFTNGIGHGVLDNHIYGETLAROKRLRFKDGKMKY 240
 QY 241 QIIDGEMYPPTVKDQAEIMYPPQVPEHLRFPAVQGEVFGVPGIMMYATTIMREHNRVCD 300
 DB 241 QIIDGEMYPPTVKDQAEIMYPPQVPEHLRFPAVQGEVFGVPGIMMYATTIMREHNRVCD 300
 QY 301 VLKQEHPEWGEOLFOFTRSLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
 DB 301 VLKQEHPEWGEOLFOFTRSLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
 QY 361 NRIAAEFNTLYHMHPLPDTFOIHDOKYNOQFIYNNSTLLEHGITQVSEFTQIAGRY 420
 DB 361 NRIAAEFNTLYHMHPLPDTFOIHDOKYNOQFIYNNSTLLEHGITQVSEFTQIAGRY 420
 QY 421 AGGRNVPAPVQKVSQASIDSRQMKYQSFNEYRRKRFMLKPYSEFEELTGKEMSALEAL 480
 DB 421 AGGRNVPAPVQKVSQASIDSRQMKYQSFNEYRRKRFMLKPYSEFEELTGKEMSALEAL 480
 QY 481 YGDIADVELYPALLVEKPRDPAIFGETMVEVGAPFSLKGMGNVICSPAYWKSTFGGEV 540
 DB 481 YGDIADVELYPALLVEKPRDPAIFGETMVEVGAPFSLKGMGNVICSPAYWKSTFGGEV 540
 QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELKIKVTINASSRSGLDIDINPTVLKER 600
 DB 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELKIKVTINASSRSGLDIDINPTVLKER 600
 QY 601 STEL 604
 DB 601 STEL 604

RESULT 6

ABU03521
 ID ABU03521 standard; protein; 604 AA.

AC ABU03521;
 DT 21-JAN-2003 (first entry)
 XX
 DE Angiogenesis-associated human protein sequence #66.
 XX
 KM Human; angiogenesis-associated transcript; angiogenesis;
 KW angiogenesis-associated disease; cancer; cytostatic.
 OS Homo sapiens.
 XX
 PN WO200279492-A2.
 PD 10-OCT-2002.
 XX
 PF 14-FEB-2002; 2002WO-US004915.
 XX
 PR 14-FEB-2001; 2001US-00784356.
 PR 22-FEB-2001; 2001US-00791390.
 PR 19-APR-2001; 2001US-0285475P.
 PR 03-AUG-2001; 2001US-0310025P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334244P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Murray R, Glynn R, Watson SR, Aziz N;
 DR WPI; 2003-040681/03.
 DR N-PSDB; ABX08805.
 XX
 PT Detecting angiogenesis-associated transcript in a cell for diagnosing and
 PT treating cancer by contacting a sample with a polynucleotide that
 PT exhibits changes in expression level as a function of time in tissue
 XX undergoing angiogenesis.

PS Example 2; Page 243; 291pp; English.

XX The present invention relates to methods and compositions for detecting
 CC an angiogenesis-associated transcript in a cell in a patient. The method
 CC involves contacting a biological sample from the patient with a
 CC polynucleotide that selectively hybridizes to a sequence at least 80%
 CC identical to any of the angiogenesis-associated human polynucleotide
 CC sequences given in the specification. These angiogenesis-associated
 CC polynucleotide sequences comprise genes that exhibit changes in
 CC expression levels as a function of time in tissue undergoing
 CC angiogenesis. The method and the polynucleotide sequences of the
 CC invention are useful for diagnosing and treating angiogenesis and
 CC angiogenesis-associated diseases e.g. cancer. The polynucleotide
 CC sequences are also useful in the gene therapy of such disorders. The
 CC angiogenesis-associated proteins encoded by the polynucleotide sequences
 CC are useful as a vaccine for therapeutic and prophylactic immunisation.
 CC ABU03521-ABU03569 represent angiogenesis-associated protein sequences
 XX

Sequence 604 AA;

Query Match 100.0%; Score 3237; DB 6; Length 604;
 Best Local Similarity 100.0%; Pred. No. 1.6e-300;
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLARALLCAVALSHSTANPCSHPCQNGVCMVGFDDYKDCDCTRTGYGNCSTPEEL 60
 DB 1 MLARALLCAVALSHSTANPCSHPCQNGVCMVGFDDYKDCDCTRTGYGNCSTPEEL 60
 QY 61 TRIKLFKPTPTVTHYIILTFKGFNNVNNIIPFLNNAISYVLTSSSHLIDSPPYNNAY 120
 DB 61 TRIKLFKPTPTVTHYIILTFKGFNNVNNIIPFLNNAISYVLTSSSHLIDSPPYNNAY 120
 QY 121 GYKSWAENSNSYTRALPVPVDDCPTPLGYVKKQKLPDSNIVEKLLRRKFIIDPQGS 180
 DB 121 GYKSWAENSNSYTRALPVPVDDCPTPLGYVKKQKLPDSNIVEKLLRRKFIIDPQGS 180
 QY 181 NMFAFFAOFHTHOFKTDHKGPAFTNGIGHGVLDNHIYGETLAROKRLRFKDGKMKY 240
 DB 181 NMFAFFAOFHTHOFKTDHKGPAFTNGIGHGVLDNHIYGETLAROKRLRFKDGKMKY 240
 QY 241 QIIDGEMYPPTVKDQAEIMYPPQVPEHLRFPAVQGEVFGVPGIMMYATTIMREHNRVCD 300
 DB 241 QIIDGEMYPPTVKDQAEIMYPPQVPEHLRFPAVQGEVFGVPGIMMYATTIMREHNRVCD 300
 QY 301 VLKQEHPEWGEOLFOFTRSLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
 DB 301 VLKQEHPEWGEOLFOFTRSLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
 QY 361 NRIAAEFNTLYHMHPLPDTFOIHDOKYNOQFIYNNSTLLEHGITQVSEFTQIAGRY 420
 DB 361 NRIAAEFNTLYHMHPLPDTFOIHDOKYNOQFIYNNSTLLEHGITQVSEFTQIAGRY 420
 QY 421 AGGRNVPAPVQKVSQASIDSRQMKYQSFNEYRRKRFMLKPYSEFEELTGKEMSALEAL 480
 DB 421 AGGRNVPAPVQKVSQASIDSRQMKYQSFNEYRRKRFMLKPYSEFEELTGKEMSALEAL 480
 QY 481 YGDIADVELYPALLVEKPRDPAIFGETMVEVGAPFSLKGMGNVICSPAYWKSTFGGEV 540
 DB 481 YGDIADVELYPALLVEKPRDPAIFGETMVEVGAPFSLKGMGNVICSPAYWKSTFGGEV 540
 QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELKIKVTINASSRSGLDIDINPTVLKER 600
 DB 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELKIKVTINASSRSGLDIDINPTVLKER 600
 QY 601 STEL 604
 DB 601 STEL 604

RESULT 7

ABR42250
 ID ABR42250 standard; protein; 604 AA.

AC ABR42250;
 XX 28-JUL-2003 (first entry)
 XX
 DE Human cyclooxygenase 2 (COX-2).
 XX
 KM Cyclooxygenase 2; COX-2; human; enzyme; vulnereary; osteopathic;
 XX gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN W02003022224-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 11-SEP-2002; 2002WO-US028930.
 XX
 PR 11-SEP-2001; 2001US-00953067.
 XX
 PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 XX
 PI O'Connor PJ;
 XX
 DR WPI: 2003-313185/30.
 XX
 DR N-PSDB; ACC57774.
 XX
 PT Novel vector useful for enhancing wound healing or treating osteoporosis,
 PT osteogenesis imperfecta, and brittle bone conditions, comprises a
 PT promoter linked to a cyclooxygenase expression cassette.
 XX
 PS Disclosure; Page 74-76; 88pp; English.
 XX
 CC The present sequence is the protein sequence of human cyclooxygenase 2
 CC (COX-2). A claimed vector for use in enhancing wound healing comprises a
 CC promoter linked to a COX expression cassette, especially encoding a COX-2
 CC gene product. The vector is used in claimed methods for enhancing wound
 CC healing and for enhancing wound healing following orthopaedic procedures.
 CC A claimed method for treating pathological heterotopic ossification,
 CC especially fibrodysplasia ossificans progressiva following hip
 CC replacement or acetabular fracture, involves administering COX-2-
 CC selective non-steroidal antiinflammatory (NSAID) drugs. The vector is
 CC also used in a claimed method for treating osteoporosis, osteogenesis
 CC imperfecta and brittle bone conditions. A claimed composition for use in
 CC wound healing comprises COX-1, COX-2 or both
 CC
 XX Sequence 604 AA;
 XX
 SQ
 Query Match 100.0%; Score 3237; DB 6; Length 604;
 Best Local Similarity 100.0%; Pred. No. 1.6e-300;
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLARALLLCVALISHTANPCSHPCNRGVCSVSGVDQKCDCTRTGFGENCSTPEFL 60
 DB 1 MLARALLLCVALISHTANPCSHPCNRGVCSVSGVDQKCDCTRTGFGENCSTPEFL 60
 QY 61 TRIKLFLKPPNTHTHYLLTHKGFNVVNNIPFLRNIMSVLTSTRSHLIDSPETYNADY 120
 DB 61 TRIKLFLKPPNTHTHYLLTHKGFNVVNNIPFLRNIMSVLTSTRSHLIDSPETYNADY 120
 QY 121 GYKSMFAFSNLSTYTRALPVPVDDCPTPLGYKGGKQLPDSNEIVEKILLRKFIPDPQGS 180
 DB 121 GYKSMFAFSNLSTYTRALPVPVDDCPTPLGYKGGKQLPDSNEIVEKILLRKFIPDPQGS 180
 QY 181 NMWFAFPAQHTHOFKTDHKGPAFTNGLGHDVNDHNIYGETLARORKLFPDGGKKY 240
 DB 181 NMWFAFPAQHTHOFKTDHKGPAFTNGLGHDVNDHNIYGETLARORKLFPDGGKKY 240
 QY 241 QIDGEMPPVYKTOAEMIPPOVPEHLRFAVGQEVGLVPGIMTYIIMLRHNRYCD 300
 DB 241 QIDGEMPPVYKTOAEMIPPOVPEHLRFAVGQEVGLVPGIMTYIIMLRHNRYCD 300
 QY 301 VLKQEHFPMGDEOLFQTSRLILIGETIKIVIEDYVQHLGSYHFKLKPDELLFNKQFOYQ 360
 DB 301 VLKQEHFPMGDEOLFQTSRLILIGETIKIVIEDYVQHLGSYHFKLKPDELLFNKQFOYQ 360

DB 301 VLKQEHFPMGDEOLFQTSRLILIGETIKIVIEDYVQHLGSYHFKLKPDELLFNKQFOYQ 360
 QY 361 NRIAEFNLLVHMHPLLPDTFQIDQKXNYOQFIYNNLSILHEGITQFVESFTQIAGRV 420
 DB 361 NRIAEFNLLVHMHPLLPDTFQIDQKXNYOQFIYNNLSILHEGITQFVESFTQIAGRV 420
 QY 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNEYRKRKFMILKPYBSFELTGKEMSALEAL 480
 DB 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNEYRKRKFMILKPYBSFELTGKEMSALEAL 480
 QY 481 YGDDIVAVELLYPALLVKEKRPDAIRGETMVEVGAPESLKGLMGVTCSPAYMKPSTFGGEV 540
 DB 481 YGDDIVAVELLYPALLVKEKRPDAIRGETMVEVGAPESLKGLMGVTCSPAYMKPSTFGGEV 540
 QY 541 GFQIINTASIQSLICNNYKGCPTFSVPDPPELLIKVTITINASSSSGLDDINPTVLLKER 600
 DB 541 GFQIINTASIQSLICNNYKGCPTFSVPDPPELLIKVTITINASSSSGLDDINPTVLLKER 600
 QY 601 STEL 604
 DB 601 STEL 604
 RESULT 8
 ADA20299
 ID ADA20299 standard; protein; 604 AA.
 XX
 AC ADA20299;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX Human cyclooxygenase 2 (COX-2) protein wild-type sequence.
 DE
 XX Cyclooxygenase 2 gene; COX 2 gene; human; arachidonic acid;
 KM prostaglandin; Pg; homeostatic function; inflammatory response;
 KM blood clotting; ovulation; bone metabolism; nerve growth; wound healing;
 KM immune response; fever; arthritis; Alzheimer's disease; osteoarthritis;
 KM bone inflammatory condition; cancer; breast cancer; COX-2 modulation;
 KM clinical response; therapeutic compound; therapeutic dose;
 XX COX-2 mediated disease; SNP; single nucleotide polymorphism; enzyme.
 XX
 OS Homo sapiens.
 XX
 EH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note="This residue can be substituted for an isoleucine
 FT as a result of a single nucleotide polymorphism"
 FT Misc-difference 275
 FT /note="This residue can be substituted for an histidine
 FT as a result of a single nucleotide polymorphism; This
 FT possible substitution is at position 275 and not 257 as
 FT stated in table 3 of the specification"
 FT Misc-difference 511
 FT /note="This residue can be substituted for an alanine as
 FT a result of a single nucleotide polymorphism"
 XX
 XX US2003082550-A1.
 PN
 XX 01-MAY-2003.
 XX
 XX 07-SEP-2001; 2001US-00949293.
 PF
 XX 08-SEP-2000; 2000US-0231250P.
 PR
 XX (THOM/) THOMANN H.
 PA (DIAM/) DIAMOND K W.
 PA (FITZ/) FITZGERALD M G.
 XX
 PI Thomann H, Diamond KW, Fitzgerald MG;
 XX WPI: 2003-596957/56.
 DR N-PSDB; ADA20274.
 XX

PT Novel polymorphic sites in cox-2 gene, useful for determining the
PT therapeutic dose of a compound in the treatment of a cox-2 mediated
PT disease.

XX Example 1; Fig 4; 23pp; English.

CC This invention relates to a novel isolated nucleic acid, including
CC polymorphic sites (single nucleotide polymorphism; SNP), which is the
CC human cyclooxygenase (COX) 2 gene. COX is the key enzyme involved in the
CC conversion of arachidonic acid to prostaglandins (PGs). PGs are involved
CC in homeostatic functions as well as inflammatory responses. Some of the
CC functions of PGs include blood clotting, ovulation, bone metabolism,
CC nerve growth, wound healing and immune responses. COX is associated with
CC various diseases, including fever, arthritis, Alzheimer's disease,
CC osteoarthritis and other bone inflammatory conditions. COX has also been
CC shown to be involved in cancer, in particular breast cancer. COX-2
CC modulation may be useful in the treatment of any of these disorders. The
CC DNA and protein sequences, including polymorphisms, of the invention may
CC be useful for predicting the clinical response to a therapeutic compound,
CC for determining the therapeutic dose of a compound in the treatment of a
CC COX-2 mediated disease, and for assessing the predisposition of an
CC individual to diseases mediated by COX-2. The present sequence is that of
CC the human COX-2 protein, encoded by the gene in which the polymorphic
CC sites (SNPs) of the invention were identified.

SQ Sequence 604 AA;

Query Match 100.0%; Score 3237; DB 7; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.6e-300;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAAALLCAVALAASHTANPCCHPCONRGVMSVGFDOYKDCCTRTGFGENCSPTPEL 60
DB 1 MAAALLCAVALAASHTANPCCHPCONRGVMSVGFDOYKDCCTRTGFGENCSPTPEL 60
QY 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPILRAIMSIVLTSSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPILRAIMSIVLTSSHLIDSPPTYNADY 120
QY 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPILRAIMSIVLTSSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPILRAIMSIVLTSSHLIDSPPTYNADY 120
QY 121 GYKSWAFNSNLSTYTRALPVPDDCPTPLGVKSKOLPDSNEIVEKLLRRFIPDPQS 180
DB 121 GYKSWAFNSNLSTYTRALPVPDDCPTPLGVKSKOLPDSNEIVEKLLRRFIPDPQS 180
QY 181 NMWAFPFQHFTHQFETDHRKGPATNGLGAVDLNHYGTLARORRLRFLKQKMKY 240
DB 181 NMWAFPFQHFTHQFETDHRKGPATNGLGAVDLNHYGTLARORRLRFLKQKMKY 240
QY 241 QIIDGEMYPPTVKDQAEIMTYPOVBEHLRFVAVGSEVREGLVGMVATIMLRHNRYCD 300
DB 241 QIIDGEMYPPTVKDQAEIMTYPOVBEHLRFVAVGSEVREGLVGMVATIMLRHNRYCD 300
QY 301 VLKQHPHWDGDFQFOTSRLLIGETIKIVIEDYVQHLSGYFKLPDELLFNKQFOYQ 360
DB 301 VLKQHPHWDGDFQFOTSRLLIGETIKIVIEDYVQHLSGYFKLPDELLFNKQFOYQ 360
QY 361 NRIAEFTILVHMHLLPDTQIHOQKNYQOFTYNNISILBHGITQVESFTROIAGRV 420
DB 361 NRIAEFTILVHMHLLPDTQIHOQKNYQOFTYNNISILBHGITQVESFTROIAGRV 420
QY 421 AGGRNVPAVQKVSQASIDSRQMKYQSFNEFRKRFMLKPYESPPELLGKEMSALEAL 480
DB 421 AGGRNVPAVQKVSQASIDSRQMKYQSFNEFRKRFMLKPYESPPELLGKEMSALEAL 480
QY 481 YGDIIDAVELVALLVEKRPDAIFGETVNEVGAPSLKGLMGVNICSPAYMKPSTFGGEV 540
DB 481 YGDIIDAVELVALLVEKRPDAIFGETVNEVGAPSLKGLMGVNICSPAYMKPSTFGGEV 540
QY 541 GFOIINTASIOSLCONVKGCPFTSFVDPDELLIKTYINTASSRSRGIDINPTVLKER 600
DB 541 GFOIINTASIOSLCONVKGCPFTSFVDPDELLIKTYINTASSRSRGIDINPTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

```

DB 601 STEL 604

RESULT 9
ID ABM78951 standard; protein; 604 AA.

AC ABM78951;

DT 15-JAN-2004 (first entry)

XX Breast cancer specific marker under-expressed in breast cancer.

KW Breast cancer; marker; prostaglandin endoperoxide synthase 2; enzyme;
KW human; diagnosis; cytosolic; biochip; vaccine.

OS Homo sapiens.

PN WO2003073911-A2.

PD 12-SEP-2003.

PF 27-FEB-2003; 2003MO-US005984.

PR 28-FEB-2002; 2002US-0359999P.

PA (GEOU) UNIV GEORGETOWN.

PI Su YA, Yang J;

DR MPI; 2003-721995/68.
DR N-PSDB; ACF79931.

PT Detecting breast cancer in a subject comprises contacting a biological
PT sample with an agent that binds to a polynucleotide or polypeptide of a
PT breast-cancer specific gene (BCSG).

PS Claim 1; Page 121-123; 143pp; English.

CC The present sequence is that of a breast cancer specific marker (BCSM)
CC encoded by a gene identified by microarray gene expression analysis as
CC being under-expressed in breast cancers in comparison to healthy tissue.
CC The BCSM was identified as prostaglandin endoperoxide synthase 2 (PTGS2).
CC This was previously reported to be undetectable in ductal carcinomas in situ.
CC carcinomas and was more likely detected in ductal carcinomas in situ.
CC PTGS2 was down-regulated in all 13 breast cancer cell lines/tissues
CC examined. It is 1 of 19 (see ABM78941-59) BCSMs of the invention that are
CC encoded by breast cancer specific genes (BCSGs) which are differentially
CC expressed in breast cancer cell lines and breast cancer tissue samples as
CC compared to control cell lines and normal tissue samples. The invention
CC provides a method for detection of breast cancer by measuring expression
CC levels of BCSGs, and in particular the level of polynucleotides
CC transcribed from and polypeptides encoded by the BCSGs. A pharmaceutical
CC composition for the treatment of breast cancer comprises a BCSM, an
CC antibody directed against a BCSM, a vaccine generated using a BCSM, or an
CC agent that modulates an expression level of a BCSG or an activity of a
CC BCSM. A biochip for diagnosing breast cancer or screening agents that
CC inhibit breast cancer comprises a BCSG or BCSM

SQ Sequence 604 AA;

Query Match 100.0%; Score 3237; DB 7; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.6e-300;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAAALLCAVALAASHTANPCCHPCONRGVMSVGFDOYKDCCTRTGFGENCSPTPEL 60
DB 1 MAAALLCAVALAASHTANPCCHPCONRGVMSVGFDOYKDCCTRTGFGENCSPTPEL 60
QY 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPILRAIMSIVLTSSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPILRAIMSIVLTSSHLIDSPPTYNADY 120

```

```

QY 121 GYKSWFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIYKLLRRKFIIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIYKLLRRKFIIDPQGS 180
QY 181 NMWFAFPAQHFTHQFKTDHKGPAFTNGLGHVLDNHYGETLARQRKLRFKDKMKY 240
DB 181 NMWFAFPAQHFTHQFKTDHKGPAFTNGLGHVLDNHYGETLARQRKLRFKDKMKY 240
QY 241 QITIDGEMYPPTVKDQAEMLYPPQVEHLRFVAGQEVFGLVPGMMYATITWLRHNRCVD 300
DB 241 QITIDGEMYPPTVKDQAEMLYPPQVEHLRFVAGQEVFGLVPGMMYATITWLRHNRCVD 300
QY 301 VIKQEHPEMGDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFEDELLFNKQFOYQ 360
DB 301 VIKQEHPEMGDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFEDELLFNKQFOYQ 360
QY 361 NRIAAEFNLTHMHPILPDTFQIHDKQXNYQCFIYNNSTILLEHGIQFVSEFTROLAGRY 420
DB 361 NRIAAEFNLTHMHPILPDTFQIHDKQXNYQCFIYNNSTILLEHGIQFVSEFTROLAGRY 420
QY 421 AGGRNVPVAVQXVSQASIDQSRQMKYQSFNEYKRRFMLEKYESFEELTGKEMSALEAL 480
DB 421 AGGRNVPVAVQXVSQASIDQSRQMKYQSFNEYKRRFMLEKYESFEELTGKEMSALEAL 480
QY 481 YGDIIDAVELYPALLVEKRPDAILFGETMVEVGAPFSLKGLMGVYICSPAYWKSTFGGEV 540
DB 481 YGDIIDAVELYPALLVEKRPDAILFGETMVEVGAPFSLKGLMGVYICSPAYWKSTFGGEV 540
QY 541 GFOIINTASTQSLICNNVKGCPFTSFVDPDELIKVTYINASSRSGLDINPTVLLKER 600
DB 541 GFOIINTASTQSLICNNVKGCPFTSFVDPDELIKVTYINASSRSGLDINPTVLLKER 600
QY 601 STEL 604
DB 601 STEL 604

```

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RESULT 10
ADD27955
ID ADD27955 standard; protein; 604 AA.
XX
AC ADD27955;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human COX-2 amino acid sequence.
XX
KW CYCLOOXYGENASE type 1; cyclooxygenase type 1 variant protein;
KW COX-1 variant protein; genetic disease; tissue typing;
KM forensic identification; COX-2.
XX
OS Homo sapiens.
XX
PN WO2003029411-A2.
XX
PD 10-APR-2003.
XX
PF 28-SEP-2002; 2002WO-US030947.
XX
PR 28-SEP-2001; 2001US-0326133P.
PR 15-APR-2002; 2002US-0373225P.
PR 16-APR-2002; 2002US-0373661P.
PR 16-SEP-2002; 2002US-0411575P.
XX
PA (UYYO ) UNIV BRIGHAM YOUNG.
XX
PI Simmons D, Chandrasekharan VN;
XX
WP; 2003-421222/39.
XX
PT Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide
PT encoding the polypeptide, useful for identifying a compound that binds to
PT and modulates the activity of COX-1 variant polypeptide.

```

```

XX Disclosure; Fig 1A; 150pp; English.
XX
CC The present invention describes an isolated cyclooxygenase type 1 (COX-1)
CC variant polypeptide (I). (I) is useful for identifying a compound which
CC modulates the activity of (I). A nucleotide sequence encoding (I) can be
CC used for mapping their respective genes on a chromosome, and so locating
CC gene regions associated with genetic disease, identifying an individual
CC from a minute biological sample (tissue typing), and to aid in forensic
CC identification of a biological sample. The present sequence represents a
CC identification which is used in the exemplification of the present invention.
XX
SQ Sequence 604 AA;

```

```

Query Match 100.0%; Score 3237; DB 7; Length 604;
Best Local Similarity 100.0%; Pred. No. 1,66-300;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLARALLCAVALASHTANPCCSHPQONRGVCMVGFQDKCDCTRTGYGNCSTPEFL 60
DB 1 MLARALLCAVALASHTANPCCSHPQONRGVCMVGFQDKCDCTRTGYGNCSTPEFL 60
QY 61 TRIKFLKPTPTVHYILTHFKGFNNVNNIPILRAIMSYLTSRSHLIDSPPTNADY 120
DB 61 TRIKFLKPTPTVHYILTHFKGFNNVNNIPILRAIMSYLTSRSHLIDSPPTNADY 120
QY 121 GYKSWFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIYKLLRRKFIIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIYKLLRRKFIIDPQGS 180
QY 181 NMWFAFPAQHFTHQFKTDHKGPAFTNGLGHVLDNHYGETLARQRKLRFKDKMKY 240
DB 181 NMWFAFPAQHFTHQFKTDHKGPAFTNGLGHVLDNHYGETLARQRKLRFKDKMKY 240
QY 241 QITIDGEMYPPTVKDQAEMLYPPQVEHLRFVAGQEVFGLVPGMMYATITWLRHNRCVD 300
DB 241 QITIDGEMYPPTVKDQAEMLYPPQVEHLRFVAGQEVFGLVPGMMYATITWLRHNRCVD 300
QY 301 VIKQEHPEMGDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFEDELLFNKQFOYQ 360
DB 301 VIKQEHPEMGDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFEDELLFNKQFOYQ 360
QY 361 NRIAAEFNLTHMHPILPDTFQIHDKQXNYQCFIYNNSTILLEHGIQFVSEFTROLAGRY 420
DB 361 NRIAAEFNLTHMHPILPDTFQIHDKQXNYQCFIYNNSTILLEHGIQFVSEFTROLAGRY 420
QY 421 AGGRNVPVAVQXVSQASIDQSRQMKYQSFNEYKRRFMLEKYESFEELTGKEMSALEAL 480
DB 421 AGGRNVPVAVQXVSQASIDQSRQMKYQSFNEYKRRFMLEKYESFEELTGKEMSALEAL 480
QY 481 YGDIIDAVELYPALLVEKRPDAILFGETMVEVGAPFSLKGLMGVYICSPAYWKSTFGGEV 540
DB 481 YGDIIDAVELYPALLVEKRPDAILFGETMVEVGAPFSLKGLMGVYICSPAYWKSTFGGEV 540
QY 541 GFOIINTASTQSLICNNVKGCPFTSFVDPDELIKVTYINASSRSGLDINPTVLLKER 600
DB 541 GFOIINTASTQSLICNNVKGCPFTSFVDPDELIKVTYINASSRSGLDINPTVLLKER 600
QY 601 STEL 604
DB 601 STEL 604

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```

RESULT 11
AAW12698
ID AAW12698 standard; protein; 604 AA.
XX
AC AAW12698;
XX
DT 04-MAY-1997 (first entry)
XX
DE Human prostaglandin H synthase-2.
XX

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KW prostaglandin H synthase-2; PGHS-2; cyclooxygenase; inflammation;
 KW pulmonary fibrosis; Alzheimer's disease; stroke; acute head injury;
 KW endometriosis; dysmenorrhea; pre-term labour; prostate cancer;
 KW colorectal cancer; squamous cell carcinoma; breast cancer;
 KW oral pharyngeal cancer; stomach cancer; fibrosarcoma; skin cancer;
 KW osteosarcoma; therapy; diagnosis.
 XX
 OS Homo sapiens.
 PN WO6640720-A1.
 PD 19-DEC-1996.
 XX
 PF 03-JUN-1996; 96WO-US008311.
 XX
 PR 07-JUN-1995; 95US-00487752.
 XX
 PA (UVRP) UNITV ROCHESTER.
 PI Young DA, O'bannon MK, Winn VD;
 XX
 DR MPI: 1997-052220/05.
 XX N-PSDB; AAT59635.
 PT Nucleic acid encoding human prostaglandin H synthase-2 - used in treating
 XX and detection of inflammation, pre-term labour, cancer, etc.
 PS
 XX Example 9; Page 84-85; 126pp; English.
 CC Human prostaglandin H synthase 2 (PGHS-2) (AA012698) is responsible for
 CC increased prostaglandin synthesis associated with inflammation. Unlike
 CC PGHS-1, expression of PGHS-2 is responsive to regulatory control. The
 CC PGHS-2 amino acid sequence was deduced from a DNA clone (AAT59635)
 CC isolated from human fibroblast W138 cells. Transfected host cells
 CC expressing human PGHS-2 can be used to identify cpts. that modulate PGHS-
 CC 2 expression and activity. Cpts. that inhibit expression may be used to
 CC treat inflammation, e.g. arterial inflammation or pulmonary fibrosis,
 CC Alzheimer's disease, stroke, acute head injury, endometriosis,
 CC dysmenorrhea, pre-term labour, cancer and radiation-induced injury.
 CC Antibodies immunospecific PGHS-2 may be used to detect PGHS-2 expression,
 CC and thus in diagnosis of certain cancers
 XX
 SQ Sequence 604 AA;
 Query Match 99.9%; Score 3234; DB 2; Length 604;
 Best Local Similarity 99.8%; Pred. No. 3.1e-300;
 Matches 603; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLARALLICAVLALSHITANPCCSHPCQNRGVCMGVGPOYKDCDCTRTGFGENGCTPFL 60
 DB 1 MLARALLICAVLALSHITANPCCSHPCQNRGVCMGVGPOYKDCDCTRTGFGENGCTPFL 60
 QY 61 TRIKFLKPTNTVHYILTFKGFNVVNNIPFLNATMSYVLSRSHLIDSPPTVNDY 120
 DB 61 TRIKFLKPTNTVHYILTFKGFNVVNNIPFLNATMSYVLSRSHLIDSPPTVNDY 120
 QY 121 GYKSWEARSNLSYTRALPVPVDDCPPLGYKQKQLPDSNEIYEKLLRRKFTPDPOGS 180
 DB 121 GYKSWEARSNLSYTRALPVPVDDCPPLGYKQKQLPDSNEIYEKLLRRKFTPDPOGS 180
 QY 121 GYKSWEARSNLSYTRALPVPVDDCPPLGYKQKQLPDSNEIYEKLLRRKFTPDPOGS 180
 DB 121 GYKSWEARSNLSYTRALPVPVDDCPPLGYKQKQLPDSNEIYEKLLRRKFTPDPOGS 180
 QY 181 NMMEFAFAQHFTFOFKTDHKGPAFTNGLGVDLNIHYETLARQKRLFDGKKKY 240
 DB 181 NMMEFAFAQHFTFOFKTDHKGPAFTNGLGVDLNIHYETLARQKRLFDGKKKY 240
 QY 241 QIIDGENYPPVKTQAEMLYPPQVPEHLRPAVQAEVGLVPGIMATYTLWRHNRYCD 300
 DB 241 QIIDGENYPPVKTQAEMLYPPQVPEHLRPAVQAEVGLVPGIMATYTLWRHNRYCD 300
 QY 301 VLKQEHMWDGEOUFOFSLILIGETIKIVIEDVYQHLSGYHFKLAKDPILLNKOPQYQ 360
 DB 301 VLKQEHMWDGEOUFOFSLILIGETIKIVIEDVYQHLSGYHFKLAKDPILLNKOPQYQ 360
 QY 361 NR1AAEFNTLYHMHPLPDTFQIHDQKXNYQOFIYNSILLEHGTQFVSEFTQIAGRV 420

DB 361 NR1AAEFNTLYHMHPLPDTFQIHDQKXNYQOFIYNSILLEHGTQFVSEFTQIAGRV 420
 QY 421 AGGRNVPVAVQKXQASIDSRQMKYQSFNEYKRFPMLKPYESFEELTGKENSALFEAL 480
 DB 421 AGGRNVPVAVQKXQASIDSRQMKYQSFNEYKRFPMLKPYESFEELTGKENSALFEAL 480
 QY 481 YGDIIDAVELYPALLVKEPRDAIFGETMVEVGAPEFSLKGLMGVYCSPAYWKPESTFGGEV 540
 DB 481 YGDIIDAVELYPALLVKEPRDAIFGETMVEVGAPEFSLKGLMGVYCSPAYWKPESTFGGEV 540
 QY 541 GFQIINTASIQSLICNNVKGCPFTSFSVPPELITKTYTINASSSRGLDINPTVLKER 600
 DB 541 GFQIINTASIQSLICNNVKGCPFTSFSVPPELITKTYTINASSSRGLDINPTVLKER 600
 QY 601 STEL 604
 DB 601 STEL 604

RESULT 12
 AARS1267
 ID AARS1267 standard; protein; 604 AA.
 XX
 AC AARS1267;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-OCT-1994 (first entry)

DE Sequence of human prostaglandin G/H synthase-2 (PGHS-2).

XX Prostaglandin; hormone; eicosanoid; fatty acid metabolism.

XX Homo sapiens.

XX WO9406919-A2.

XX 31-MAR-1994.

XX 22-SEP-1993; 93WO-US009167.

XX 22-SEP-1992; 92US-00949780.

XX 01-DEC-1992; 92US-00983835.

XX 22-MAR-1993; 93US-00034143.

XX 28-APR-1993; 93US-00054364.

XX (UVRP) UNITV ROCHESTER.

XX Young DA, O'bannon MK, Winn VD;

XX MPI: 1994-118468/14.

XX N-PSDB; AA061790.

XX New prostaglandin G/H synthase-2 gene - used for producing transgenic
 PT cell lines for testing ability of cpts. to inhibit synthesis of
 PT prostaglandin(s).

XX Claim 40; Page 45-47; 76pp; English.

XX RNA was isolated from a human fibroblast cell line (W138). PCR primers
 CC specific for the human PGHS-1 and PGHS-2 sequences were engineered to
 CC amplify the coding regions of either one transcript or the other (see
 CC AA061792-95). PCR products of about 2 kb were generated. Three PGHS-2
 CC clones were sequenced in both directions. The clone comprising the PGHS-2
 CC sequence disclosed in AA061790 was selected for transfection. This
 CC sequence differs from the human PGHS-2 sequence disclosed by Hla and
 CC Hellson, PNAS, 89, 7384 (1992) due to a Glu rather than a Gly at AA posn.
 CC 165. Mouse PGHS-2 also has a Glu at this posn. (Updated on 25-MAR-2003 to
 CC correct FN field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 604 AA;

Query Match 97.0%; Score 3140; DB 2; Length 604;

Best Local Similarity 97.4%; Pred. No. 3.1e-291;
Matches 588; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

```

QY 1 MLARLLCAVALASHTANPCCSHPCONRGVCMGVGFQYKDCDCTRTGFGNCSPTPEL 60
Db 1 MLARLLCAVALASHTANPCCSHPCONRGVCMGVGFQYKDCDCTRTGFGNCSPTPEL 60
QY 61 TRIKFLKPTNTVHYIILTHEKGFNNVNNIPELNNALMSYVLTSRSHLIDSPPTYNADY 120
Db 61 TRIKFLKPTNTVHYIILTHEKGFNNVNNIPELNNALMSYVLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWSEAFNLSYTRALPPVDDCPPIGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
Db 121 GYKSWSEAFNLSYTRALPPVDDCPPIGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
QY 181 NMFEAFQHTHOFKTDHKGPAFTNGIGHVDLNIYGETLARQRKLRFKDGKMKY 240
Db 181 NMFEAFQHTHOFKTDHKGPAFTNGIGHVDLNIYGETLARQRKLRFKDGKMKY 240
QY 241 QIIDGEMVPPYKDTQAEKITPPQVPEHLRFVGVGEVGLVGLMMVATIMLRHNRYCD 300
Db 241 QIIDGEMVPPYKDTQAEKITPPQVPEHLRFVGVGEVGLVGLMMVATIMLRHNRYCD 300
QY 301 VKQHPHEWDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHPKLFKDELLFNKQFOYQ 360
Db 301 VKQHPHEWDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHPKLFKDELLFNKQFOYQ 360
QY 361 NR1AAEFNTLYMHPLLPDTFOIHDQKYNVQCFIYNNLSILHEGITQFVESFTROJAGV 420
Db 361 NR1AAEFNTLYMHPLLPDTFOIHDQKYNVQCFIYNNLSILHEGITQFVESFTROJAGV 420
QY 421 AGGRNPPVAVQKYSQASIDQSRQKQSFNRYKRMKPYSEFELTGKMSALEAL 480
Db 421 AGGRNPPVAVQKYSQASIDQSRQKQSFNRYKRMKPYSEFELTGKMSALEAL 480
QY 481 YGDIIDVELYPAALVEKRPDAIFGETMVEVGAFFSLKGLMGVNICSPAYMKPSTFGGEV 540
Db 481 YGDIIDVELYPAALVEKRPDAIFGETMVEVGAFFSLKGLMGVNICSPAYMKPSTFGGEV 540
QY 541 GFOIINTASIOSLICNNVKCPTSFSPDPBELIKVTIINASSRSGLDINDPTVLKER 600
Db 541 GFOIINTASIOSLICNNVKCPTSFSPDPBELIKVTIINASSRSGLDINDPTVLKER 600
QY 601 STEL 604
Db 601 STEL 604

```

RESULT 13
AAV29649 standard; protein; 553 AA.

AAV29649;
19-OCT-1999 (first entry)

Human prostaglandin H2 synthase Sbjct protein.
H-ras; HIV-1; reverse transcriptase; prostaglandin H2 synthase; PGRS-2;
protein folding inhibitor; PFI; growth; proliferation; drug.

Homo sapiens.
MO9940435-A1.
12-AUG-1999.
06-FEB-1999; 99MO-US002612.
09-FEB-1998; 98US-0074070P.
(NETZ/) NETZER W J.

Pf Netzer WJ;
XX WPI: 1999-508524/42.
XX Methods for discovery, development and use of drugs and drug lead
XX molecules that inhibit protein folding.
XX Example: Page 37-38; 116pp; English.

The present invention describes the identification of protein folding inhibitors (PFI) by determining the ratio of unfolded to folded protein in the presence and absence of a test compound under protein biosynthetic conditions after stress. Identifying PFI comprises: (i) contacting a protein biosynthetic system under protein synthesis conditions with at least one test compound; and (ii) determining whether the test compound increases the ratio of unfolded protein to folded protein, where an increase in the ratio is indicative that the test compound is a PFI. The method can be used for the discovery, development and use of drugs and drug lead molecules that inhibit protein folding. The inhibitors identified can be used in methods to inhibit cellular action of a protein by inhibiting de novo folding in vivo, and optionally in conjunction with heat shock treatment. The inhibitors can be used to modulate cellular processes, e.g., enhancing the immunogenicity of a peptide or protein. The inhibitors can modulate growth or proliferation of a cell by inhibiting irreversible folding of the protein target. The tests can be carried out using a wide range of procedures therefore making the detection more simple and flexible for the operator. The present sequence represents human prostaglandin H2 synthase (PGRS-2) used in the exemplification of the present invention

Sequence 553 AA;

Query Match 92.4%; Score 2992; DB 2; Length 553;
Best Local Similarity 99.8%; Pred. No. 4.1e-277;
Matches 552; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 19 NPCCSHPCONRGVCMGVGFQYKDCDCTRTGFGNCSPTPELRIKLPNTVHYIIL 78
Db 1 NPCCSHPCONRGVCMGVGFQYKDCDCTRTGFGNCSPTPELRIKLPNTVHYIIL 60
QY 79 THKGFNNVNNIPELNNALMSYVLTSRSHLIDSPPTYNADYGYKSWSEAFNLSYTRAL 138
Db 79 THKGFNNVNNIPELNNALMSYVLTSRSHLIDSPPTYNADYGYKSWSEAFNLSYTRAL 120
QY 61 THKGFNNVNNIPELNNALMSYVLTSRSHLIDSPPTYNADYGYKSWSEAFNLSYTRAL 120
Db 61 THKGFNNVNNIPELNNALMSYVLTSRSHLIDSPPTYNADYGYKSWSEAFNLSYTRAL 120
QY 139 PVPDDCPTPIGVKGGKQLPDSNEIVEKLLRRKFIPDPGSGNMFEAFQHTHOFKFT 198
Db 139 PVPDDCPTPIGVKGGKQLPDSNEIVEKLLRRKFIPDPGSGNMFEAFQHTHOFKFT 180
QY 199 DHRGPAFTNGIGHVDLNIYGETLARQRKLRFKDGKMKYQIIDGEMVPPYKDTQAE 256
Db 199 DHRGPAFTNGIGHVDLNIYGETLARQRKLRFKDGKMKYQIIDGEMVPPYKDTQAE 240
QY 259 MTPPOVPEHLRFVGVGEVGLVGLMMVATIMLRHNRYCDVLKQHPHEWDEQLFQTS 318
Db 259 MTPPOVPEHLRFVGVGEVGLVGLMMVATIMLRHNRYCDVLKQHPHEWDEQLFQTS 300
QY 319 RLILIGETIKIVIEDYVQHLSGYHPKLFKDELLFNKQFOYQNR1AAEFNTLYMHPLLP 378
Db 319 RLILIGETIKIVIEDYVQHLSGYHPKLFKDELLFNKQFOYQNR1AAEFNTLYMHPLLP 360
QY 379 DTFQIHDQKYNVQCFIYNNLSILHEGITQFVESFTROJAGVAGGRNPPVAVQKYSQASI 438
Db 379 DTFQIHDQKYNVQCFIYNNLSILHEGITQFVESFTROJAGVAGGRNPPVAVQKYSQASI 420
QY 439 DQSRQKQSFNRYKRMKPYSEFELTGKMSALEALYGDIDAVELYPALVEKP 498
Db 439 DQSRQKQSFNRYKRMKPYSEFELTGKMSALEALYGDIDAVELYPALVEKP 480
QY 499 RPDALFGETMVEVGAFFSLKGLMGVNICSPAYMKPSTFGGEVGRQIINTASIOSLICNNV 558
Db 499 RPDALFGETMVEVGAFFSLKGLMGVNICSPAYMKPSTFGGEVGRQIINTASIOSLICNNV 540
QY 559 KGCPFTSGVDP 571

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Db          541 KGCFSTSFVDP 553
|||||
RESULT 14
ID ABB07248 standard; protein; 604 AA.
XX
AC ABB07248;
XX
DT 26-MAR-2002 (first entry)
XX
DE Rabbit cyclooxygenase-2 (COX-2) protein.
XX
KW Cyclooxygenase; COX-1; COX-2; canine; arthritis; cancer; neoplasia;
XX inflammation; central nervous system; rabbit.
OS Oryctolagus cuniculus.
XX
PN M020011026-A1.
XX
PD 15-FEB-2001.
XX
PF 04-AUG-2000; 2000MO-US019565.
XX
PR 06-AUG-1999; 99US-0147601P.
XX
PA (SEAR ) SEARLE & CO G D.
XX
PI Gierse JK;
XX
DR WPI; 2002-113777/15.
XX
PT Novel substantially purified canine cyclooxygenase 1 or 2 protein, useful
XX for identifying drugs that can reduce inflammation in dogs, and screening
XX selective inhibitors of cyclooxygenase-2 protein.
XX
PS Disclosure; Fig 3; 122pp; English.
XX
CC The invention relates to genes that encode canine cyclooxygenase (COX)-1
XX or COX-2 proteins. The COX proteins, especially COX-2 is useful for
XX diagnosing or prognosing a COX-2 related condition in a dog. COX-2 or its
XX fragment is useful for identifying a test material which has the ability
XX to inhibit, suppress, modulate, or maintain canine COX-2 activity. The
XX COX-1 and COX-2 polynucleotides are useful for determining an association
XX between a polymorphism and a trait. COX-2 cDNA molecules and methods
XX provided are also useful for diagnosing or prognosing an association
XX condition such as arthritis, cancer, neoplasia, inflammation or central
XX nervous system disorder in a dog. The present sequence represents a
XX rabbit COX-2 protein, used in comparison studies with the canine COX-2
XX
SQ Sequence 604 AA:
Query Match          91.8%; Score 2971; DB 5; Length 604;
Best Local Similarity 89.9%; Pred. No. 4.8e-275;
Matches 543; Conservative 35; Mismatches 26; Indels 0; Gaps 0;
QY 1 MLARALLCAVLAISHANPCCHPCNRCVCMVGFDQYKDCDCTRTGFYGENCSTPEFL 60
Db 1 MLARALLCAAVLAISHANPCCHPCNRCVCMVGFDQYKDCDCTRTGFYGENCSTPEFL 60
QY 61 TRIKLFLKPTPNTHVYLLTHFKGPMNVNIIPLRNALIMSYVLTSSHLIDSEPTYNADY 120
Db 61 TRIKLFLKPTPNTHVYLLTHFKGPMNVNIIPLRNALIMSYVLTSSHLIDSEPTYNADY 120
QY 121 GYSWMAFSNLISYTRALPVPDPDCEPTLGVKGGKQOLPDSNETVEKLLRRKRTIPQGS 180
Db 121 GYSWMAFSNLISYTRALPVPDPDCEPTLGVKGGKQOLPDSNETVEKLLRRKRTIPQGS 180
QY 121 NYKSWMAFSNLISYTRALPVPADCEPTPMGVKKGKELPSKDVVEKLLRRKRTIPDQGT 180
Db 121 NYKSWMAFSNLISYTRALPVPADCEPTPMGVKKGKELPSKDVVEKLLRRKRTIPDQGT 180
QY 181 NMMAFAFAQHTTQCFKTHKRGPAFTNGIGSHGVNDINHLYGRTIARQRLTLFKDGKMKY 240
Db 181 NMMAFAFAQHTTQCFKTHKRGPAFTNGIGSHGVNDINHLYGRTIARQRLTLFKDGKMKY 240

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QY 241 QIIDGEMYPRTVKDQTAEMTYPPQVEHLRFANQGEVGLVPGIMMYATIMLRHNRCVD 300
Db 241 QVIDGEVYPPPTVKDQTAEMTYPPHIAHQFAVQGEVGLVPGIMMYATIMLRHNRCVD 300
QY 301 VLKQEHPEWDEQLFQTSRLILIGETIKTIVEDYVQHLSCYHNRKAKRDEPLLKNQFOYQ 360
Db 301 VLKQEHPEWDEQLFQTSRLILIGETIKTIVEDYVQHLSCYHNRKAKRDEPLLKNQFOYQ 360
QY 361 NRJAEFNTLYHWHPLLPDTFQIHQKYNVQCFIYNNISILDEGITQFVSEFTROLAGRY 420
Db 361 NRJAEFNTLYHWHPLLPDTFQIHQKYNVQCFIYNNISILDEGITQFVSEFTROLAGRY 420
QY 421 AGGRNVPVAVQKASIDQSRQKYSQSNREYRKRFMLPYSEFEELTGKEMASLEAL 480
Db 421 AGGRNVPVAVQKASIDQSRQKYSQSNREYRKRFMLPYSEFEELTGKEMASLEAL 480
QY 481 YGDIDAVELYPALLVKKPRPDALFGEITWEVGAPELKGIMNVITCSPAWKESTGGEV 540
Db 481 YGDIDAVELYPALLVKKPRPDALFGEITWEVGAPELKGIMNVITCSPAWKESTGGEV 540
QY 541 GFQIINTASTQSLICNNVKGCEFTSFVDPDELIKTIVTINASSRSGLDINDPTVLLKGR 600
Db 541 GFQIINTASTQSLICNNVKGCEFTSFVDPDELIKTIVTINASSRSGLDINDPTVLLKGR 600
QY 601 STEL 604
Db 601 STEL 604

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RESULT 15
ADD27960
ID ADD27960 standard; protein; 604 AA.
XX
AC ADD27960;
XX
DT 15-JAN-2004 (first entry)
XX
DE Rabbit COX-2 amino acid sequence.
XX
KW cyclooxygenase type 1; cyclooxygenase type 1 variant protein;
XX forensic identification; COX-2.
XX
OS Oryctolagus cuniculus.
XX
PN M02003029411-A2.
XX
PD 10-APR-2003.
XX
PF 28-SEP-2002; 2002MO-US030947.
XX
PR 28-SEP-2001; 2001US-0326133P.
XX
PR 15-APR-2002; 2002US-0373225P.
XX
PR 16-APR-2002; 2002US-0373661P.
XX
PR 16-SEP-2002; 2002US-0411575P.
XX
PA (UYYO ) UNIV BRIGHAM YOUNG.
XX
PI Simmons D, Chandrasekharan VN;
XX
DR WPI; 2003-421222/39.
XX

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Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide encoding the polypeptide, useful for identifying a compound that binds to and modulates the activity of COX-1 variant polypeptide.

Disclosure; Fig 1A; 150pp; English.

The present invention describes an isolated cyclooxygenase type 1 (COX-1) variant polypeptide (1). (1) is useful for identifying a compound which modulates the activity of (1). A nucleotide sequence encoding (1) can be used for mapping their respective genes on a chromosome, and so locating gene regions associated with genetic disease, identifying an individual

CC from a minute biological sample (tissue typing), and to aid in forensic
 CC identification of a biological sample. The present sequence represents a
 CC sequence which is used in the exemplification of the present invention.

XX
 SO Sequence 604 AA;

Query Match 91.8%; Score 2971; DB 7; Length 604;

Best Local Similarity 89.9%; Pred. No. 4.8e-275;
 Matches 543; Conservative 35; Mismatches 26; Indels 0; Gaps 0;

```

QY 1 MLARALLICAVLALSHSTANPCSHPCQNRGVCMGVGPDQYKCDCTRTGFGYENGCTBEFL 60
Db 1 MLARALLICAVLALSHSTANPCSHPCQNRGVCMGVGPDQYKCDCTRTGFGYENGCTBEFL 60
QY 61 TRIKLFKPTNTVHYIITHFKGFWNVNNIPEFLNAIMSVLTSRSLIDSPPTYNADY 120
Db 61 TRIKLFKPTNTVHYIITHFKGFWNVNNIPEFLNAIMSVLTSRSLIDSPPTYNADY 120
QY 121 GYKSWAENSLSYTRALPVYDCCPTLGVKGGKOLPDSNEIYEKLLRRKFIPTDPOGS 180
Db 121 GYKSWAENSLSYTRALPVYDCCPTLGVKGGKOLPDSNEIYEKLLRRKFIPTDPOGS 180
QY 121 NYKSWAENSLSYTRALPVYDCCPTLGVKGGKOLPDSNEIYEKLLRRKFIPTDPOGS 180
Db 121 NYKSWAENSLSYTRALPVYDCCPTLGVKGGKOLPDSNEIYEKLLRRKFIPTDPOGS 180
QY 181 NMFAFPAQHFTQPFKTDHKKGPAFTNGLGHVLDNHIYGETLARQRRLFKDGKMKY 240
Db 181 NMFAFPAQHFTQPFKTDHKKGPAFTNGLGHVLDNHIYGETLARQRRLFKDGKMKY 240
QY 241 QIIDSEMYPTVYKDTQAEIYPPQVEHILRFVAVGQEVFGVLPGLMMYATITWLEHNRVCD 300
Db 241 QIIDSEMYPTVYKDTQAEIYPPQVEHILRFVAVGQEVFGVLPGLMMYATITWLEHNRVCD 300
QY 301 VIKQHPREMGDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFKDPPELLFNKQFOYQ 360
Db 301 VIKQHPREMGDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFKDPPELLFNKQFOYQ 360
QY 361 NRFAEFNTLYMHPLLPDPTFOIHQKXNYQOPIYNNISILLEGITQFVESFTROLAGRY 420
Db 361 NRFAEFNTLYMHPLLPDPTFOIHQKXNYQOPIYNNISILLEGITQFVESFTROLAGRY 420
QY 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNEVYKRPMLKPYESFEELTGEKEMAELEAL 480
Db 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNEVYKRPMLKPYESFEELTGEKEMAELEAL 480
QY 481 YGIDAVELYPALVEKPRPDALFGEIWEVGAFFSLKGLMGNVICSPAYMKPSTFGGEV 540
Db 481 YGIDAVELYPALVEKPRPDALFGEIWEVGAFFSLKGLMGNVICSPAYMKPSTFGGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFPDPELIKVTYTNASSRSGLDINPTVLKER 600
Db 541 GFOIINTASIOSLICNNVKGCPFTSFPDPELIKVTYTNASSRSGLDINPTVLKER 600
QY 601 STEL 604
Db 601 STEL 604

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Search completed: April 24, 2004, 07:19:19
 Job time : 81 secs

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OM protein - protein search, using sw model

Run on: April 24, 2004, 07:17:00 ; Search time 25 Seconds

(without alignments)
1247.283 Million cell updates/secTitle: US-08-064-271-10
Perfect score: 3237

Sequence: 1 MBLALLCAVLAHSHTAMP.....RSGLDINPTVILKERSTEL 604

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3237	100.0	604	1	US-08-064-271-10
2	3237	100.0	604	2	US-08-487-753-4
3	3237	100.0	604	3	US-08-480-065-4
4	3237	100.0	604	3	US-08-487-744-4
5	3237	100.0	604	3	US-08-930-589A-18
6	3237	100.0	604	4	US-09-599-781-18
7	3237	100.0	604	5	PCT-US93-09167-4
8	3230	99.8	604	2	US-08-487-753-5
9	3230	99.8	604	2	US-08-480-065-5
10	3230	99.8	604	3	US-08-487-744-5
11	3230	99.8	604	4	PCT-US93-09167-5
12	2967	91.7	604	5	US-09-919-060-5
13	2873	88.8	604	1	US-08-487-753-2
14	2873	88.8	604	2	US-08-480-065-2
15	2873	88.8	604	3	US-08-487-744-2
16	2873	88.8	604	5	PCT-US93-09167-2
17	2029.5	62.7	633	4	US-09-919-060-13
18	885	27.3	180	4	US-09-919-060-2
19	313	9.7	91	4	US-09-919-060-10
20	225	7.0	913	3	US-08-911-853-17
21	225	7.0	913	3	US-09-479-409-17
22	225	7.0	913	4	US-09-479-453-17
23	160.5	5.0	933	2	US-08-313-200-1
24	160.5	5.0	933	4	US-09-251-039-2
25	160.5	5.0	933	5	PCT-US93-03837-1
26	160	4.9	1551	4	US-09-437-568A-46
27	149.5	4.6	695	6	5460961-5

28	115	3.6	3135	1	US-08-323-170B-2	Sequence 2, Appli
29	115	3.6	3135	4	US-08-954-441-2	Sequence 2, Appli
30	112	3.5	667	4	US-09-107-532A-3749	Sequence 3749, Ap
31	110.5	3.4	1525	3	US-09-191-647-2	Sequence 2, Appli
32	110.5	3.4	1525	3	US-09-540-245A-2	Sequence 2, Appli
33	110.5	3.4	1525	3	US-09-540-153-2	Sequence 2, Appli
34	109	3.4	2471	1	US-08-185-432-16	Sequence 16, Appli
35	109	3.4	2471	1	US-08-083-590A-19	Sequence 19, Appli
36	109	3.4	2471	3	US-08-532-384-19	Sequence 19, Appli
37	109	3.4	2471	4	US-08-899-232-1	Sequence 1, Appli
38	108.5	3.4	661	1	US-08-375-709-3	Sequence 3, Appli
39	108.5	3.4	1075	1	US-07-623-033-2	Sequence 2, Appli
40	108.5	3.4	1075	1	US-08-514-975B-2	Sequence 2, Appli
41	108.5	3.4	2165	1	US-08-514-975B-2	Sequence 2, Appli
42	108.5	3.4	2165	5	PCT-US95-12507-2	Sequence 2, Appli
43	107.5	3.3	1529	4	US-09-312-283C-396	Sequence 396, App
44	107	3.3	543	4	US-09-328-352-7396	Sequence 7396, Ap
45	107	3.3	559	4	US-09-672-749-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-064-271-10
Sequence 10, Application US/08064271

Patent No. 5543297

GENERAL INFORMATION:

APPLICANT: Kennedy, Brian P.

APPLICANT: Cromlish, Wanda A.

APPLICANT: Mancini, Joseph A.

APPLICANT: O'Neill, Gary J.

APPLICANT: Vickers, Philip J.

TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 cDNA AND

NUMBER OF SEQUENCES: 14

ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 Lincoln Avenue

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 in, 1.4kb

COMPUTER: Apple Macintosh

OPERATING SYSTEM: System 7

SOFTWARE: Microsoft Word 5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/064,271

FILING DATE: 19930506

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Panzer, Curtis C.

REGISTRATION NUMBER: 33,752

REFERENCE/DOCKET NUMBER: 189061A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908)594-3199

TELEFAX: (908)594-4720

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 604 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-064-271-10

Query Match 100.0%; Score 3237; DB 1; Length 604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLARALLICAVIALSHTANPCCSHPCQNRGYCMGVGFQYKDCDCTRTGFGYGCSTPEFL 60
 DB 1 MLARALLICAVIALSHTANPCCSHPCQNRGYCMGVGFQYKDCDCTRTGFGYGCSTPEFL 60
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 DB 61 TRIKFLKPTENTVHYILTHEKGFNNVNNIPEFLNALSIVLTSRSHLIDSPPTYNADY 120
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 DB 121 GYKSWAEPNSLSYTRALPVPDDCPTPLGVYKQKQLPDSNEIVEKLLRRKFIPDPQS 180
 QY 181 NMMPFAFQHFTHQFETDKHKGPAFTNGLGHVLDNHIYGETLARORRLRFLKQGMKY 240
 DB 181 NMMPFAFQHFTHQFETDKHKGPAFTNGLGHVLDNHIYGETLARORRLRFLKQGMKY 240
 QY 241 QIIDGEMPTVKDQAEIYPPQVEHLRFVAGQEVFELVGLMMYATIMLRHNRYCD 300
 DB 241 QIIDGEMPTVKDQAEIYPPQVEHLRFVAGQEVFELVGLMMYATIMLRHNRYCD 300
 QY 301 VLKQHEPWEQDQFQTSRLIIGETIKIVIEDYVQHSYHFKLKEPDELLFNKQFOYQ 360
 DB 301 VLKQHEPWEQDQFQTSRLIIGETIKIVIEDYVQHSYHFKLKEPDELLFNKQFOYQ 360
 QY 361 NR1AAEFNTLYHMHPLPDTFQIHQKXNYQCFIYNNLSILHGIQFVESFTROLAGRY 420
 DB 361 NR1AAEFNTLYHMHPLPDTFQIHQKXNYQCFIYNNLSILHGIQFVESFTROLAGRY 420
 QY 421 AGGRNVPAPVQKVSQASIDQSRQMKYQSFNEYKRFMLKPYESFEELTGKESABELEAL 480
 DB 421 AGGRNVPAPVQKVSQASIDQSRQMKYQSFNEYKRFMLKPYESFEELTGKESABELEAL 480
 QY 481 YGDIIDAVELYPALVKEPRPDALFGETMVEVGAFFSLKGLMGVITCSPAYWKSTFGGEV 540
 DB 481 YGDIIDAVELYPALVKEPRPDALFGETMVEVGAFFSLKGLMGVITCSPAYWKSTFGGEV 540
 QY 541 GFOIINTASIQSLICNNVKGCPTSFVDPPELKITVTINASSRSGLDINFTVLKER 600
 DB 541 GFOIINTASIQSLICNNVKGCPTSFVDPPELKITVTINASSRSGLDINFTVLKER 600
 QY 601 STEL 604
 DB 601 STEL 604
 RESULT 2
 US-08-487-753-4
 ; Sequence 4, Application US/08487753
 ; Patent No. 5807733
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Donald A.
 ; APPLICANT: O'Banion, Michael K.
 ; APPLICANT: Winn, Virginia D.
 ; TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
 ; TITLE OF INVENTION: FUSION PROTEINS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,753
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 3996-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 604 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-487-753-4
 Query Match 100.0%; Score 3237; DB 1; Length 604;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLARALLICAVIALSHTANPCCSHPCQNRGYCMGVGFQYKDCDCTRTGFGYGCSTPEFL 60
 DB 1 MLARALLICAVIALSHTANPCCSHPCQNRGYCMGVGFQYKDCDCTRTGFGYGCSTPEFL 60
 QY 61 TRIKFLKPTENTVHYILTHEKGFNNVNNIPEFLNALSIVLTSRSHLIDSPPTYNADY 120
 DB 61 TRIKFLKPTENTVHYILTHEKGFNNVNNIPEFLNALSIVLTSRSHLIDSPPTYNADY 120
 QY 121 GYKSWAEPNSLSYTRALPVPDDCPTPLGVYKQKQLPDSNEIVEKLLRRKFIPDPQS 180
 DB 121 GYKSWAEPNSLSYTRALPVPDDCPTPLGVYKQKQLPDSNEIVEKLLRRKFIPDPQS 180
 QY 181 NMMPFAFQHFTHQFETDKHKGPAFTNGLGHVLDNHIYGETLARORRLRFLKQGMKY 240
 DB 181 NMMPFAFQHFTHQFETDKHKGPAFTNGLGHVLDNHIYGETLARORRLRFLKQGMKY 240
 QY 241 QIIDGEMPTVKDQAEIYPPQVEHLRFVAGQEVFELVGLMMYATIMLRHNRYCD 300
 DB 241 QIIDGEMPTVKDQAEIYPPQVEHLRFVAGQEVFELVGLMMYATIMLRHNRYCD 300
 QY 301 VLKQHEPWEQDQFQTSRLIIGETIKIVIEDYVQHSYHFKLKEPDELLFNKQFOYQ 360
 DB 301 VLKQHEPWEQDQFQTSRLIIGETIKIVIEDYVQHSYHFKLKEPDELLFNKQFOYQ 360
 QY 361 NR1AAEFNTLYHMHPLPDTFQIHQKXNYQCFIYNNLSILHGIQFVESFTROLAGRY 420
 DB 361 NR1AAEFNTLYHMHPLPDTFQIHQKXNYQCFIYNNLSILHGIQFVESFTROLAGRY 420
 QY 421 AGGRNVPAPVQKVSQASIDQSRQMKYQSFNEYKRFMLKPYESFEELTGKESABELEAL 480
 DB 421 AGGRNVPAPVQKVSQASIDQSRQMKYQSFNEYKRFMLKPYESFEELTGKESABELEAL 480
 QY 481 YGDIIDAVELYPALVKEPRPDALFGETMVEVGAFFSLKGLMGVITCSPAYWKSTFGGEV 540
 DB 481 YGDIIDAVELYPALVKEPRPDALFGETMVEVGAFFSLKGLMGVITCSPAYWKSTFGGEV 540
 QY 541 GFOIINTASIQSLICNNVKGCPTSFVDPPELKITVTINASSRSGLDINFTVLKER 600
 DB 541 GFOIINTASIQSLICNNVKGCPTSFVDPPELKITVTINASSRSGLDINFTVLKER 600
 QY 601 STEL 604
 DB 601 STEL 604
 RESULT 3
 US-08-480-065-4
 ; Sequence 4, Application US/08480065
 ; Patent No. 5837479
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Donald A.
 ; APPLICANT: O'Banion, Michael K.
 ; APPLICANT: Winn, Virginia D.

```

/ TITLE OF INVENTION: SCREENIN ASSAYS FOR INHIBITORS OF
/ TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,065
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 3996-012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELETYPE: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 604 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-480-065-4

Query Match      100.0%; Score 3237; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M1ARALLCAVALALSHANPCSHPCONRGVMSVGFDOYKDCRTGTGFGNCSTPEFL 60
DB 1 M1ARALLCAVALALSHANPCSHPCONRGVMSVGFDOYKDCRTGTGFGNCSTPEFL 60
QY 61 TRIKFLKPTPTVHYIILTHKGFVNANNIPFLNAINSVYLTSRSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTPTVHYIILTHKGFVNANNIPFLNAINSVYLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWFAFNSNLSYTRALPVPDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPODGS 180
DB 121 GYKSWFAFNSNLSYTRALPVPDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPODGS 180
QY 181 NMFAFPAQHFTQHFKEKDPATNGLGHGVDLNIYGETLARQRKRLFKDGKMKY 240
DB 181 NMFAFPAQHFTQHFKEKDPATNGLGHGVDLNIYGETLARQRKRLFKDGKMKY 240
QY 241 QIIDEMPTPTVKTQAEWITPPQVEHLRFVGVGEVFGVLGMVYATITWLRHNRCVD 300
DB 241 QIIDEMPTPTVKTQAEWITPPQVEHLRFVGVGEVFGVLGMVYATITWLRHNRCVD 300
QY 301 VIKQHPHPEQDEQLQTSRLILIGETIKIVIEDYVQHSNGHFKLKPDELLFNKQFOYQ 360
DB 301 VIKQHPHPEQDEQLQTSRLILIGETIKIVIEDYVQHSNGHFKLKPDELLFNKQFOYQ 360
QY 361 NRIAEFNTLYMHMLDPTFOIHQKYNVQOFTNNLSLLEHGIITQFVESTRLQIAGV 420
DB 361 NRIAEFNTLYMHMLDPTFOIHQKYNVQOFTNNLSLLEHGIITQFVESTRLQIAGV 420
QY 421 AGGRVNPVAVQVQASIDQSRQMYQSFNEVYRKFPMKPYBSFELLTGEKEMSALEAL 480
DB 421 AGGRVNPVAVQVQASIDQSRQMYQSFNEVYRKFPMKPYBSFELLTGEKEMSALEAL 480
QY 481 YGDIDAVELYPALLVEKRPDAIFGETWVEVGAFFSLGMLGNVTCSPAYMKPSTFGGEV 540

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DB 481 YGDIDAVELYPALLVEKRPDAIFGETWVEVGAFFSLGMLGNVTCSPAYMKPSTFGGEV 540
QY 541 GFOIINTASTQSLICNNKCCPTSFVDPDEHLIKVTYINASSRSSGLDINPTVLKER 600
DB 541 GFOIINTASTQSLICNNKCCPTSFVDPDEHLIKVTYINASSRSSGLDINPTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

RESULT 4
US-08-487-744-4
/ Sequence 4: Application US/08487744
/ Patent No. 6048850
/ GENERAL INFORMATION:
/ APPLICANT: Young, Donald A.
/ APPLICANT: O'Banion, Michael K.
/ APPLICANT: Winn, Virginia D.
/ TITLE OF INVENTION: METHODS FOR INHIBITING PROSTAGLANDIN
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/487,744
/ FILING DATE:
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 3996-013
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELETYPE: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 604 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-487-744-4

Query Match      100.0%; Score 3237; DB 3; Length 604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M1ARALLCAVALALSHANPCSHPCONRGVMSVGFDOYKDCRTGTGFGNCSTPEFL 60
DB 1 M1ARALLCAVALALSHANPCSHPCONRGVMSVGFDOYKDCRTGTGFGNCSTPEFL 60
QY 61 TRIKFLKPTPTVHYIILTHKGFVNANNIPFLNAINSVYLTSRSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTPTVHYIILTHKGFVNANNIPFLNAINSVYLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWFAFNSNLSYTRALPVPDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPODGS 180
DB 121 GYKSWFAFNSNLSYTRALPVPDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPODGS 180
QY 181 NMFAFPAQHFTQHFKEKDPATNGLGHGVDLNIYGETLARQRKRLFKDGKMKY 240

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/599,781
FILING DATE: 21-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/084,033
FILING DATE: 27-Sep-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coppola, Joseph A
REGISTRATION NUMBER: 38,413
REFERENCE/DOCKET NUMBER: 19029PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-6734
TELEFAX: 732-594-4720
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-599-781-18

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Query Match      100.0%; Score 3237; DB 4; Length 604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLARALLICAVALLSHSTANPCSHPCONRGVCMVSGVDFDYKDDCTRTGFGYGCSTPEEL 60
DB 1 MLARALLICAVALLSHSTANPCSHPCONRGVCMVSGVDFDYKDDCTRTGFGYGCSTPEEL 60
QY 61 TRIKFLKPTPTVTHYILTHFKGFNVVNNIPFLRNAINSYVLTSRSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTPTVTHYILTHFKGFNVVNNIPFLRNAINSYVLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWAFAFNSLYTRALPVDPDCTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 180
DB 121 GYKSWAFAFNSLYTRALPVDPDCTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 180
QY 181 NMMFAFAQHFTHOEFKTDHKGPAFTNGLGHGVDLNHIYGETLAROKRLRFKGGKMY 240
DB 181 NMMFAFAQHFTHOEFKTDHKGPAFTNGLGHGVDLNHIYGETLAROKRLRFKGGKMY 240
QY 241 QIIDGEMTPPYKTDQAEIMYPPQVPEHLRFVQGEVFGVLVGLMMYATIMLRHNRYCD 300
DB 241 QIIDGEMTPPYKTDQAEIMYPPQVPEHLRFVQGEVFGVLVGLMMYATIMLRHNRYCD 300
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DB 301 VIKQHPHMGDEQLQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
QY 361 NRIAAEFNTLYEMHPLPDTFOIHDQKYNVQOFIYNNSTILFHGITOFESETRQIAGV 420
DB 361 NRIAAEFNTLYEMHPLPDTFOIHDQKYNVQOFIYNNSTILFHGITOFESETRQIAGV 420
QY 421 AGGRVVPRAVQVQASIDQSFOMKYQSFNEYRKRPFMLKPYSPFELTGEKEMSAELAL 480
DB 421 AGGRVVPRAVQVQASIDQSFOMKYQSFNEYRKRPFMLKPYSPFELTGEKEMSAELAL 480
QY 481 YGDIIDAVELYPALVLEKRPDAIFGETMVEVAPPSLGLMGWNVICSPAYKPESTFGGEV 540
DB 481 YGDIIDAVELYPALVLEKRPDAIFGETMVEVAPPSLGLMGWNVICSPAYKPESTFGGEV 540
QY 541 GFQIINTASIOSLICNNVKGCPFTSFVDDPELLIKTVITINASSSSGDDINPTVLLKER 600
DB 541 GFQIINTASIOSLICNNVKGCPFTSFVDDPELLIKTVITINASSSSGDDINPTVLLKER 600

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QY 601 STEL 604
DB 601 STEL 604

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RESULT 7
PCT-US93-09167-4
Sequence 4, Application PC/TUS9309167
GENERAL INFORMATION:
APPLICANT: Young, Donald A.
APPLICANT: O'Banion, M. Kerry
APPLICANT: Winn, Virginia D.
TITLE OF INVENTION: Stably-Transformed Mammalian Cells
TITLE OF INVENTION: Expressing a Regulated, Inflammatory Cyclooxygenase
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 Norwest Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09167
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 8840.20-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Amino acid sequence for Human PGHS-2
PCT-US93-09167-4

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Query Match      100.0%; Score 3237; DB 5; Length 604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLARALLICAVALLSHSTANPCSHPCONRGVCMVSGVDFDYKDDCTRTGFGYGCSTPEEL 60
QY 61 TRIKFLKPTPTVTHYILTHFKGFNVVNNIPFLRNAINSYVLTSRSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTPTVTHYILTHFKGFNVVNNIPFLRNAINSYVLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWAFAFNSLYTRALPVDPDCTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 180
DB 121 GYKSWAFAFNSLYTRALPVDPDCTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 180
QY 181 NMMFAFAQHFTHOEFKTDHKGPAFTNGLGHGVDLNHIYGETLAROKRLRFKGGKMY 240
DB 181 NMMFAFAQHFTHOEFKTDHKGPAFTNGLGHGVDLNHIYGETLAROKRLRFKGGKMY 240
QY 241 QIIDGEMTPPYKTDQAEIMYPPQVPEHLRFVQGEVFGVLVGLMMYATIMLRHNRYCD 300
DB 241 QIIDGEMTPPYKTDQAEIMYPPQVPEHLRFVQGEVFGVLVGLMMYATIMLRHNRYCD 300

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QY 301 VLKQHEPWEQDQFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKFDELLFNKQFOYQ 360
 DB 301 VLKQHEPWEQDQFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKFDELLFNKQFOYQ 360
 QY 361 NRIAAEFNTLYHMHPLPDTFQIHQKXNYQOFTYNNLSILHEGHTQFVESFTROLAGRY 420
 DB 361 NRIAAEFNTLYHMHPLPDTFQIHQKXNYQOFTYNNLSILHEGHTQFVESFTROLAGRY 420
 QY 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNEYKRKRMFLKPYSEFELTGKEMSALEAL 480
 DB 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNEYKRKRMFLKPYSEFELTGKEMSALEAL 480
 QY 481 YGDIADVELYPALVYKRPDPAIFGETMVEVGAFFSLKGLMGVICSAPYWKSTFGGEV 540
 DB 481 YGDIADVELYPALVYKRPDPAIFGETMVEVGAFFSLKGLMGVICSAPYWKSTFGGEV 540
 QY 541 GFOIINTASTOSLICNNVKGCPFTSFVDPPELIKVTITINASSRSGLDINFTVLKER 600
 DB 541 GFOIINTASTOSLICNNVKGCPFTSFVDPPELIKVTITINASSRSGLDINFTVLKER 600
 QY 601 STEL 604
 DB 601 STEL 604

RESULT 8

US-08-487-753-5
 ; Sequence 5, Application US/08487753
 ; Patent No. 5807733
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Donald A.
 ; APPLICANT: O'Banion, Michael K.
 ; APPLICANT: Winn, Virginia D.
 ; TITLE OF INVENTION: MAMMALIAN PROTAGLANDIN H SYNTHASE-2
 ; TITLE OF INVENTION: FUSION PROTEINS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennle & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,753
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 3996-011
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 604 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-487-753-5

Query Match 99.8%; Score 3230; DB 1; Length 604;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 603; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLARALLCAVALASHTANPCCSHPCONRGVMSVGFQYKCDCTRTGFGYGENCSTPEL 60
 DB 1 MLARALLCAVALASHTANPCCSHPCONRGVMSVGFQYKCDCTRTGFGYGENCSTPEL 60
 QY 61 TRIKFLKPTENTVHYILTHFKGFNNVYNNITPELNAIMSYL7SRSHLIDSPPTYNADY 120
 DB 61 TRIKFLKPTENTVHYILTHFKGFNNVYNNITPELNAIMSYL7SRSHLIDSPPTYNADY 120
 QY 121 GYKSWAEPNSLSYTRALBPVDDCPTPLGVGKKQLPDSNIEVEKLLRRRFPDPQGS 180
 DB 121 GYKSWAEPNSLSYTRALBPVDDCPTPLGVGKKQLPDSNIEVEKLLRRRFPDPQGS 180
 QY 181 NMFFAFAHFTHQFETDHRKGPATNGIGHVDLNIYGETLARQRKLRFKQGMKY 240
 DB 181 NMFFAFAHFTHQFETDHRKGPATNGIGHVDLNIYGETLARQRKLRFKQGMKY 240
 QY 241 QIIDGEMPPYKDTQAEKITPPQVPEHLRFVAGQEVFGLVGLMMYATITWLEHNRVCD 300
 DB 241 QIIDGEMPPYKDTQAEKITPPQVPEHLRFVAGQEVFGLVGLMMYATITWLEHNRVCD 300
 QY 301 VLKQHEPWEQDQFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKFDELLFNKQFOYQ 360
 DB 301 VLKQHEPWEQDQFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKFDELLFNKQFOYQ 360
 QY 361 NRIAAEFNTLYHMHPLPDTFQIHQKXNYQOFTYNNLSILHEGHTQFVESFTROLAGRY 420
 DB 361 NRIAAEFNTLYHMHPLPDTFQIHQKXNYQOFTYNNLSILHEGHTQFVESFTROLAGRY 420
 QY 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNEYKRKRMFLKPYSEFELTGKEMSALEAL 480
 DB 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNEYKRKRMFLKPYSEFELTGKEMSALEAL 480
 QY 481 YGDIADVELYPALVYKRPDPAIFGETMVEVGAFFSLKGLMGVICSAPYWKSTFGGEV 540
 DB 481 YGDIADVELYPALVYKRPDPAIFGETMVEVGAFFSLKGLMGVICSAPYWKSTFGGEV 540
 QY 541 GFOIINTASTOSLICNNVKGCPFTSFVDPPELIKVTITINASSRSGLDINFTVLKER 600
 DB 541 GFOIINTASTOSLICNNVKGCPFTSFVDPPELIKVTITINASSRSGLDINFTVLKER 600
 QY 601 STEL 604
 DB 601 STEL 604

RESULT 9

US-08-480-065-5
 ; Sequence 5, Application US/08480065
 ; Patent No. 5837479
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Donald A.
 ; APPLICANT: O'Banion, Michael K.
 ; APPLICANT: Winn, Virginia D.
 ; TITLE OF INVENTION: SCREENIN ASSAYS FOR INHIBITORS OF
 ; TITLE OF INVENTION: MAMMALIAN PROTAGLANDIN H SYNTHASE-2
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennle & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,065
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

Db 481 YGDDAVELYPALLVEKRPDAIFGETWVEGAPSLKGMGNVICSAPYWKPFSTFGGEV 540
 QY 541 GFOIINTASIOSLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPTVLKER 600
 Db 541 GFOIINTASIOSLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPTVLKER 600
 QY 601 STEL 604
 Db 601 STEL 604

RESULT 11

PCT-US93-09167-5
 ; Sequence 5, Application PC/TUS9309167
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Donald A.
 ; APPLICANT: O'Banion, M. Kerry
 ; APPLICANT: Winn, Virginia D.
 ; TITLE OF INVENTION: Stably-Transformed Mammalian Cells
 ; TITLE OF INVENTION: Expressing a Regulated, Inflammatory Cyclooxygenase
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 3100 Northwest Center
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/09167
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Moessner, Warren D.
 ; REGISTRATION NUMBER: 30,440
 ; REFERENCE/DOCKET NUMBER: 8840.20-US-01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-332-5300
 ; TELEFAX: 612-332-9081
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 604 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: Amino acid sequence Human PGHS-2
 ; PCT-US93-09167-5

Query Match 99.8%; Score 3230; DB 5; Length 604;

Best Local Similarity 99.8%; Pred. No. 0; Indels 0; Gaps 0;

Matches 603; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLARALLCAVALASHNTANPCSSHPCQNRGVCMGVGFDQYKCDCTRTGFGYENGSTPEFL 60
 Db 1 MLARALLCAVALASHNTANPCSSHPCQNRGVCMGVGFDQYKCDCTRTGFGYENGSTPEFL 60
 QY 61 TRIKLFKPTNTVHYILTHFKGFVNWNINPFLRNAMSYVLTSRSHLIDSPPTYNADY 120
 Db 61 TRIKLFKPTNTVHYILTHFKGFVNWNINPFLRNAMSYVLTSRSHLIDSPPTYNADY 120
 QY 121 GYKSWAEFNSNLSYTRALPVPDDCPTPLGVKGKKQLPDSNEIYEKLLRRKFTIPDPGGS 180
 Db 121 GYKSWAEFNSNLSYTRALPVPDDCPTPLGVKGKKQLPDSNEIYEKLLRRKFTIPDPGGS 180
 QY 181 NMFAFFAQHFTHQPFKTDHKGPAFTNGLGHVLDNHIYGETLARQKRLFKDGKMKY 240

Db 181 NMFAFFAQHFTHQPFKTDHKGPAFTNGLGHVLDNHIYGETLARQKRLFKDGKMKY 240
 QY 241 QIIDGEMVPPVTKTOEMITPPOVPEHLRPAVGQEVGLVGLMMYATIMLRHNRYCD 300
 Db 241 QIIDGEMVPPVTKTOEMITPPOVPEHLRPAVGQEVGLVGLMMYATIMLRHNRYCD 300
 QY 301 VLKQHPPEWDEQLFOTSRLLIGRTIKIVIEDVYQHLSGYFKLKPDELLFNKQFOYQ 360
 Db 301 VLKQHPPEWDEQLFOTSRLLIGRTIKIVIEDVYQHLSGYFKLKPDELLFNKQFOYQ 360
 QY 361 NRIAAEFNTLYHMLPDPDTQIHDQKNYQOFTYNNLSLLEHGTQVESFTQIAGRV 420
 Db 361 NRIAAEFNTLYHMLPDPDTQIHDQKNYQOFTYNNLSLLEHGTQVESFTQIAGRV 420
 QY 421 AGGRVVPVAVQKVSQASIDQSRQKXQSFNERKRFMLKPYESPPELLTGEKMSALEAL 480
 Db 421 AGGRVVPVAVQKVSQASIDQSRQKXQSFNERKRFMLKPYESPPELLTGEKMSALEAL 480
 QY 481 YGDDAVELYPALLVEKRPDAIFGETWVEGAPSLKGMGNVICSAPYWKPFSTFGGEV 540
 Db 481 YGDDAVELYPALLVEKRPDAIFGETWVEGAPSLKGMGNVICSAPYWKPFSTFGGEV 540
 QY 541 GFOIINTASIOSLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPTVLKER 600
 Db 541 GFOIINTASIOSLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPTVLKER 600
 QY 601 STEL 604
 Db 601 STEL 604

RESULT 12

US-09-919-060-5
 ; Sequence 5, Application US/09919060
 ; Patent No. 6639744
 ; GENERAL INFORMATION:
 ; APPLICANT: Wisniewski, Nancy
 ; APPLICANT: Brandt, Kevin S.
 ; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
 ; FILE REFERENCE: AD-1
 ; CURRENT APPLICATION NUMBER: US/09/919,060
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: 60/224,486
 ; PRIOR FILING DATE: 2000-08-11
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patent In version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 604
 ; TYPE: PRT
 ; ORGANISM: Canis familiaris
 ; US-09-919-060-5

Query Match 91.7%; Score 2967; DB 4; Length 604;

Best Local Similarity 90.1%; Pred. No. 5.6e-298;

Matches 544; Conservative 30; Mismatches 30; Indels 0; Gaps 0;

QY 1 MLARALLCAVALASHNTANPCSSHPCQNRGVCMGVGFDQYKCDCTRTGFGYENGSTPEFL 60
 Db 1 MLARALLCAVALASHNTANPCSSHPCQNRGVCMGVGFDQYKCDCTRTGFGYENGSTPEFL 60
 QY 61 TRIKLFKPTNTVHYILTHFKGFVNWNINPFLRNAMSYVLTSRSHLIDSPPTYNADY 120
 Db 61 TRIKLFKPTNTVHYILTHFKGFVNWNINPFLRNAMSYVLTSRSHLIDSPPTYNADY 120
 QY 121 GYKSWAEFNSNLSYTRALPVPDDCPTPLGVKGKKQLPDSNEIYEKLLRRKFTIPDPGGS 180
 Db 121 GYKSWAEFNSNLSYTRALPVPDDCPTPLGVKGKKQLPDSNEIYEKLLRRKFTIPDPGGS 180
 QY 181 NMFAFFAQHFTHQPFKTDHKGPAFTNGLGHVLDNHIYGETLARQKRLFKDGKMKY 240
 Db 181 NMFAFFAQHFTHQPFKTDHKGPAFTNGLGHVLDNHIYGETLARQKRLFKDGKMKY 240

QY 241 QIIDGEMYPPTVKDQOAEMLYPPQVEHLRPAVGQEVGVLVPGIMVATITWLRHNRYCD 300
 Db 241 QVIDGEVYPTVKDQOAEMLYPPQVEHLRPAVGQEVGVLVPGIMVATITWLRHNRYCD 300
 QY 301 VLKQEHPEWDEQOLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFKQFOYQ 360
 Db 301 VLKQEHPEWDEQOLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFKQFOYQ 360
 QY 361 NRIAEENLYHMHPLPDTFQIHDOXNYQOFTYNNSSILLEGITQFVESFTQJAGRY 420
 Db 361 NRIAEENLYHMHPLPDTFQIHDOXNYQOFTYNNSSILLEGITQFVESFTQJAGRY 420
 QY 421 AGGRNVPAAVQAKASIDQSRQMKYOSFNEVYKRPMLKPYSPFEELTGKEMSALEAL 480
 Db 421 AGGRNVPAAVQAKASIDQSRQMKYOSFNEVYKRPMLKPYSPFEELTGKEMSALEAL 480
 QY 481 YGIDAVELYPALVEKRPDAIFGETMVEGAPFSLKGLMGNVCSPAYMKSTFGGEV 540
 Db 481 YGIDAVELYPALVEKRPDAIFGETMVEGAPFSLKGLMGNVCSPAYMKSTFGGEV 540
 QY 541 GFOIINTASIOSLICNNVGCPTSFVSVPDELLIKVTINASSRSGLDINPTVLLKER 600
 Db 541 GFOIINTASIOSLICNNVGCPTSFVSVPDELLIKVTINASSRSGLDINPTVLLKER 600
 QY 601 STEL 604
 Db 601 STEL 604

RESULT 13

US-08-487-753-2
 ; Sequence 2, Application US/08487753
 ; Patent No. 5807733

GENERAL INFORMATION:

APPLICANT: Young, Donald A.
 APPLICANT: O'Banion, Michael K.
 TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
 TITLE OF INVENTION: FUSION PROTEINS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESS: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,753
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 3996-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/88864
 TELETYPE: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 604 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-487-753-2

Query Match

88.8%; Score 2873; DB 1; Length 604;

Best Local Similarity 86.8%; Pred. No. 3e-288;
 Matches 524; Conservative 39; Mismatches 41; Indels 0; Gaps 0;

QY 1 MLRALILCALVALASHTANPCSHPCONRGVCSVGFQYKCDCTRGTGFCNCSPTPEFL 60
 Db 1 MLRAVLCAALGLSQAANPCSNPCONRGVCSVGFQYKCDCTRGTGFCNCSPTPEFL 60
 QY 61 TRIKLKLKPPNTVHYILTHFKGFKNVNNIPPLRNALMSYVLTSSRLIDSPPTVADY 120
 Db 61 TRIKLKLKPPNTVHYILTHFKGFKNVNNIPPLRNALMSYVLTSSRLIDSPPTVADY 120
 QY 121 GYSWAEFSLSYTTALPVPDDCPTLGVKKKQOLPDSNEVEYKLLLRKRTIPDQGS 180
 Db 121 GYSWAEFSLSYTTALPVPDDCPTLGVKKKQOLPDSNEVEYKLLLRKRTIPDQGS 180
 QY 181 NMFAFAQFHTHOFKTDHKGPAFTNGLSGVLDNLHLYGETLARQKRLFKDGKLY 240
 Db 181 NMFAFAQFHTHOFKTDHKGPAFTNGLSGVLDNLHLYGETLARQKRLFKDGKLY 240
 QY 241 QIIDGEMYPPTVKDQOAEMLYPPQVEHLRPAVGQEVGVLVPGIMVATITWLRHNRYCD 300
 Db 241 QIIDGEMYPPTVKDQOAEMLYPPQVEHLRPAVGQEVGVLVPGIMVATITWLRHNRYCD 300
 QY 301 VLKQEHPEWDEQOLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFKQFOYQ 360
 Db 301 VLKQEHPEWDEQOLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFKQFOYQ 360
 QY 361 NRIAEENLYHMHPLPDTFQIHDOXNYQOFTYNNSSILLEGITQFVESFTQJAGRY 420
 Db 361 NRIAEENLYHMHPLPDTFQIHDOXNYQOFTYNNSSILLEGITQFVESFTQJAGRY 420
 QY 421 AGGRNVPAAVQAKASIDQSRQMKYOSFNEVYKRPMLKPYSPFEELTGKEMSALEAL 480
 Db 421 AGGRNVPAAVQAKASIDQSRQMKYOSFNEVYKRPMLKPYSPFEELTGKEMSALEAL 480
 QY 481 YGIDAVELYPALVEKRPDAIFGETMVEGAPFSLKGLMGNVCSPAYMKSTFGGEV 540
 Db 481 YGIDAVELYPALVEKRPDAIFGETMVEGAPFSLKGLMGNVCSPAYMKSTFGGEV 540
 QY 541 GFOIINTASIOSLICNNVGCPTSFVSVPDELLIKVTINASSRSGLDINPTVLLKER 600
 Db 541 GFOIINTASIOSLICNNVGCPTSFVSVPDELLIKVTINASSRSGLDINPTVLLKER 600
 QY 601 STEL 604
 Db 601 STEL 604

RESULT 14

US-08-480-065-2
 ; Sequence 2, Application US/08480065
 ; Patent No. 5837479

GENERAL INFORMATION:

APPLICANT: Young, Donald A.
 APPLICANT: O'Banion, Michael K.
 TITLE OF INVENTION: SCREENING ASSAYS FOR INHIBITORS OF
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESS: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,065

FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 3996-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELETYPE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 604 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-480-065-2

Query Match 88.8%; Score 2873; DB 2; Length 604;
 Best Local Similarity 86.8%; Pred. No. 3e-288;
 Matches 524; Conservative 39; Mismatches 41; Indels 0; Gaps 0;

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QY 1 MLARALLCAVALALSHANTANPCSSHPCCNKGVCMSVGFDDYKCDCTRTGFGYGENCSFPEFL 60
DB 1 MLFRAVLICAAALGSLQAANPCSSNPGCCNKGVCMSVGFDDYKCDCTRTGFGYGENCSFPEFL 60
QY 61 TRIKFLKPTENTVHYILTHFKGFMNVNNIPFLRNALMSYVLTSSHLIDSPPTYNADY 120
DB 61 TRIKLLKPTENTVHYILTHFKGFMNVNNIPFLRNALMSYVLTSSHLIDSPPTYNADY 120
QY 121 GYKSWAFAFNLSTYTRALPPVADDCPTPGVGKGNKELPSKKEVLEKVLRRRPIPDQGS 180
DB 121 GYKSWAFAFNLSTYTRALPPVADDCPTPGVGKGNKELPSKKEVLEKVLRRRPIPDQGS 180
QY 121 GYKSWAFAFNLSTYTRALPPVADDCPTPGVGKGNKELPSKKEVLEKVLRRRPIPDQGS 180
DB 121 GYKSWAFAFNLSTYTRALPPVADDCPTPGVGKGNKELPSKKEVLEKVLRRRPIPDQGS 180
QY 181 NMFAFAFHQFTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLARQKRLFKDGKMY 240
DB 181 NMFAFAFHQFTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLARQKRLFKDGKMY 240
QY 181 NMFAFAFHQFTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLARQKRLFKDGKMY 240
DB 181 NMFAFAFHQFTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLARQKRLFKDGKMY 240
QY 241 QIIDGEMYPPTVKDTQAEMLYPPQVPEHLRFAYGQEVFGIVPGIMATYATLWLEHNRVCD 300
DB 241 QIIDGEMYPPTVKDTQAEMLYPPQVPEHLRFAYGQEVFGIVPGIMATYATLWLEHNRVCD 300
QY 241 QVIGGEVYPTVKDTQAEMLYPPQVPEHLRFAYGQEVFGIVPGIMATYATLWLEHNRVCD 300
DB 241 QVIGGEVYPTVKDTQAEMLYPPQVPEHLRFAYGQEVFGIVPGIMATYATLWLEHNRVCD 300
QY 301 VLKQEHPEWDEQLFQTSRLILGETIKIYIEDYVQHLSGYHFKLKDPELLFNQGFQYQ 360
DB 301 VLKQEHPEWDEQLFQTSRLILGETIKIYIEDYVQHLSGYHFKLKDPELLFNQGFQYQ 360
QY 301 ILKQEHPEWDEQLFQTSRLILGETIKIYIEDYVQHLSGYHFKLKDPELLFNQGFQYQ 360
DB 301 ILKQEHPEWDEQLFQTSRLILGETIKIYIEDYVQHLSGYHFKLKDPELLFNQGFQYQ 360
QY 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYQOFTYNNISILLEGITQFVESFTROIAGRV 420
DB 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYQOFTYNNISILLEGITQFVESFTROIAGRV 420
QY 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYQOFTYNNISILLEGITQFVESFTROIAGRV 420
DB 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYQOFTYNNISILLEGITQFVESFTROIAGRV 420
QY 421 AGGRNVPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYTSFEEITGKEMAELEAL 480
DB 421 AGGRNVPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYTSFEEITGKEMAELEAL 480
QY 421 AGGRNVPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYTSFEEITGKEMAELEAL 480
DB 421 AGGRNVPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYTSFEEITGKEMAELEAL 480
QY 481 YGSDIDAEVLPALVVEKPRDPAIFGETMVEGAPFSLKGLMGVYICSPAYMKSTFEGEV 540
DB 481 YGSDIDAEVLPALVVEKPRDPAIFGETMVEGAPFSLKGLMGVYICSPAYMKSTFEGEV 540
QY 541 GFQIINTASIQSLICNNVKGCPFTSFVPPDELIKIYITINASSRSGLDINPVLAKR 600
DB 541 GFQIINTASIQSLICNNVKGCPFTSFVPPDELIKIYITINASSRSGLDINPVLAKR 600
QY 601 STEL 604
DB 601 STEL 604

```

RESULT 15
 US-08-487-744-2
 Sequence 2, Application US/08487744
 Patent No. 6048850
 GENERAL INFORMATION:
 APPLICANT: Young, Donald A.

APPLICANT: O'Banion, Michael K.
 APPLICANT: Winn, Virginia D.
 TITLE OF INVENTION: METHODS FOR INHIBITING PROSTAGLANDIN
 TITLE OF INVENTION: SYNTHESIS IN A MAMMALIAN HOST
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,744
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 3996-013
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELETYPE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 604 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-487-744-2

Query Match 88.8%; Score 2873; DB 3; Length 604;
 Best Local Similarity 86.8%; Pred. No. 3e-288;
 Matches 524; Conservative 39; Mismatches 41; Indels 0; Gaps 0;

```

QY 1 MLARALLCAVALALSHANTANPCSSHPCCNKGVCMSVGFDDYKCDCTRTGFGYGENCSFPEFL 60
DB 1 MLFRAVLICAAALGSLQAANPCSSNPGCCNKGVCMSVGFDDYKCDCTRTGFGYGENCSFPEFL 60
QY 61 TRIKFLKPTENTVHYILTHFKGFMNVNNIPFLRNALMSYVLTSSHLIDSPPTYNADY 120
DB 61 TRIKLLKPTENTVHYILTHFKGFMNVNNIPFLRNALMSYVLTSSHLIDSPPTYNADY 120
QY 121 GYKSWAFAFNLSTYTRALPPVADDCPTPGVGKGNKELPSKKEVLEKVLRRRPIPDQGS 180
DB 121 GYKSWAFAFNLSTYTRALPPVADDCPTPGVGKGNKELPSKKEVLEKVLRRRPIPDQGS 180
QY 121 GYKSWAFAFNLSTYTRALPPVADDCPTPGVGKGNKELPSKKEVLEKVLRRRPIPDQGS 180
DB 121 GYKSWAFAFNLSTYTRALPPVADDCPTPGVGKGNKELPSKKEVLEKVLRRRPIPDQGS 180
QY 181 NMFAFAFHQFTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLARQKRLFKDGKMY 240
DB 181 NMFAFAFHQFTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLARQKRLFKDGKMY 240
QY 181 NMFAFAFHQFTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLARQKRLFKDGKMY 240
DB 181 NMFAFAFHQFTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLARQKRLFKDGKMY 240
QY 241 QIIDGEMYPPTVKDTQAEMLYPPQVPEHLRFAYGQEVFGIVPGIMATYATLWLEHNRVCD 300
DB 241 QIIDGEMYPPTVKDTQAEMLYPPQVPEHLRFAYGQEVFGIVPGIMATYATLWLEHNRVCD 300
QY 241 QVIGGEVYPTVKDTQAEMLYPPQVPEHLRFAYGQEVFGIVPGIMATYATLWLEHNRVCD 300
DB 241 QVIGGEVYPTVKDTQAEMLYPPQVPEHLRFAYGQEVFGIVPGIMATYATLWLEHNRVCD 300
QY 301 VLKQEHPEWDEQLFQTSRLILGETIKIYIEDYVQHLSGYHFKLKDPELLFNQGFQYQ 360
DB 301 VLKQEHPEWDEQLFQTSRLILGETIKIYIEDYVQHLSGYHFKLKDPELLFNQGFQYQ 360
QY 301 ILKQEHPEWDEQLFQTSRLILGETIKIYIEDYVQHLSGYHFKLKDPELLFNQGFQYQ 360
DB 301 ILKQEHPEWDEQLFQTSRLILGETIKIYIEDYVQHLSGYHFKLKDPELLFNQGFQYQ 360
QY 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYQOFTYNNISILLEGITQFVESFTROIAGRV 420
DB 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYQOFTYNNISILLEGITQFVESFTROIAGRV 420
QY 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYQOFTYNNISILLEGITQFVESFTROIAGRV 420
DB 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYQOFTYNNISILLEGITQFVESFTROIAGRV 420
QY 421 AGGRNVPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYTSFEEITGKEMAELEAL 480
DB 421 AGGRNVPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYTSFEEITGKEMAELEAL 480
QY 421 AGGRNVPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYTSFEEITGKEMAELEAL 480
DB 421 AGGRNVPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYTSFEEITGKEMAELEAL 480

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Sun Apr 25 18:03:17 2004

us-08-064-271-10.ra1

Page 11

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QY 481 YSDIDAVELYPALVKEKPPDDAIFGSETWVEGAPFSLKIGMGNVICSPAYWKSTPGEV 540
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 481 YSDIDAVELYPALVKEKPPDDAIFGSETWVEGAPFSLKIGMGNVICSPAYWKSTPGEV 540
QY 541 GFOIINTASIOSLGNWVGCPFTSRVDPDELKTVTINASSRSGLDINPTVLKRR 600
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 541 GFKIINTASIOSLGNWVGCPFTSRVDPDELKTVTINASSRSGLDINPTVLKRR 600
QY 601 STEL 604
    : : : : :
Db 601 STEL 604
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Search completed: April 24, 2004, 07:22:09
Job time : 27 secs

8/10/21

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 24, 2004, 07:21:12 ; Search time 73 seconds
(without alignments)
2287.548 Million cell updates/sec

Title: US-08-064-271-10

Perfect score: 3237

Sequence: 1 MARRALLCAVLAISHTPANP.....RSGLDINPTVTLKERSTEL 604

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1133595 segs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3237	100.0	604	10	US-09-953-067A-4
2	3237	100.0	604	10	US-09-949-293-33
3	3237	100.0	604	12	US-10-211-462-133
4	3237	100.0	604	12	US-10-170-385-237
5	3237	100.0	604	14	US-10-027-961A-18
6	3237	100.0	604	14	US-10-021-660-109
7	3237	100.0	604	15	US-10-260-937-22
8	3237	100.0	604	15	US-10-295-027-32
9	3237	100.0	604	15	US-10-373-801-30
10	2971	91.8	604	15	US-10-260-937-27
11	2967	91.7	604	9	US-09-919-060-5
12	2958	90.8	604	10	US-09-949-293-30
13	2938	90.3	604	15	US-10-260-937-26
14	2923	90.3	604	15	US-10-260-937-25
15	2902	89.7	599	10	US-09-949-293-31

16	2892	89.3	604	10	US-09-949-293-28	Sequence 28, Appl
17	2892	89.3	604	15	US-10-260-937-28	Sequence 26, Appl
18	2881.5	89.0	603	10	US-09-949-293-32	Sequence 32, Appl
19	2881.5	89.0	603	15	US-10-260-937-23	Sequence 23, Appl
20	2881.5	89.0	603	15	US-10-260-937-24	Sequence 24, Appl
21	2877	88.9	604	10	US-09-949-293-26	Sequence 26, Appl
22	2873	88.8	604	15	US-10-260-937-29	Sequence 29, Appl
23	2868	88.6	604	15	US-09-953-067A-8	Sequence 8, Appl
24	2868	88.6	604	15	US-10-260-937-30	Sequence 30, Appl
25	2828	87.4	604	15	US-10-260-937-46	Sequence 46, Appl
26	2741	84.7	582	15	US-10-260-937-35	Sequence 35, Appl
27	2726.5	84.2	603	15	US-10-260-937-31	Sequence 31, Appl
28	2629	81.2	544	10	US-09-949-293-29	Sequence 29, Appl
29	2525	78.0	544	10	US-09-949-293-27	Sequence 27, Appl
30	2425	74.9	607	15	US-10-260-937-33	Sequence 33, Appl
31	2417	74.7	607	15	US-10-260-937-32	Sequence 32, Appl
32	2045.5	63.2	599	10	US-09-953-067A-3	Sequence 3, Appl
33	2037	62.9	599	12	US-10-382-248-6	Sequence 6, Appl
34	2037	62.9	599	12	US-10-382-248-6	Sequence 6, Appl
35	2037	62.9	599	14	US-10-097-340-264	Sequence 264, App
36	2037	62.9	599	15	US-10-260-937-47	Sequence 47, Appl
37	2036.5	62.9	602	15	US-10-260-937-52	Sequence 52, Appl
38	2035.5	62.9	629	15	US-10-260-937-15	Sequence 15, Appl
39	2029.5	62.7	632	15	US-10-260-937-60	Sequence 60, Appl
40	2029.5	62.7	633	9	US-09-919-060-13	Sequence 13, Appl
41	2029.5	62.7	633	15	US-10-260-937-2	Sequence 2, Appl
42	2027.5	62.6	602	15	US-09-953-067A-7	Sequence 7, Appl
43	2027.5	62.6	602	15	US-10-260-937-51	Sequence 51, Appl
44	2026.5	62.6	603	15	US-10-260-937-58	Sequence 58, Appl
45	2024.5	62.5	598	15	US-10-260-937-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1

US-09-953-067A-4

Sequence 4, Application US/09953067A

Publication No. US20030082141A1

GENERAL INFORMATION:

APPLICANT: O'CONNOR, J. Patrick

TITLE OF INVENTION: COX-2 FUNCTION AND WOUND HEALING

FILE REFERENCE: 267/043

CURRENT APPLICATION NUMBER: US/09/953,067A

CURRENT FILING DATE: 2001-09-11

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 604

TYPE: PRT

ORGANISM: Homo sapiens

US-09-953-067A-4

Query Match 100.0%; Score 3237; DB 10; Length 604;
Best Local Similarity 100.0%; Pred. No. 6.1e-313;
Matches 604; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MARRALLCAVLAISHTPANPCCHPQNRGVCMVSGFDQKDCRTGTGFGNCSTPEFL	60
DB	1	MARRALLCAVLAISHTPANPCCHPQNRGVCMVSGFDQKDCRTGTGFGNCSTPEFL	60
QY	61	TRIKLFLKPTPTVTHILTHFGFMVNNIPPLRAIMSVYLTSSHLIDSPPTNADY	120
DB	61	TRIKLFLKPTPTVTHILTHFGFMVNNIPPLRAIMSVYLTSSHLIDSPPTNADY	120
QY	121	GYSKMEAFSNLSYTRALPPVDDCPTPLGVKSKOLPDSNEIVKLLLRKFIIPPOGS	180
DB	121	GYSKMEAFSNLSYTRALPPVDDCPTPLGVKSKOLPDSNEIVKLLLRKFIIPPOGS	180
QY	181	NNMFAFAQHPTHPQFKTKHKGPAFTNGLGHCVDNHTYGETLARQKRLRFKDGKMY	240
DB	181	NNMFAFAQHPTHPQFKTKHKGPAFTNGLGHCVDNHTYGETLARQKRLRFKDGKMY	240

Qy	241	QIIDGEMPPYKOTQAMITPPOVPEHLIRAVQGEVPGLVPGIMYATITMREHRVD	300
Db	241	QIIDGEMPPYKOTQAMITPPOVPEHLIRAVQGEVPGLVPGIMYATITMREHRVD	300
Qy	301	VKQSEHPMGDEQLFQTSRLITIGTTIKIVIEDVVOHLSGVHFLKJRPPELLFNKQFOYO	360
Db	301	VKQSEHPMGDEQLFQTSRLITIGTTIKIVIEDVVOHLSGVHFLKJRPPELLFNKQFOYO	360
Qy	361	NRIAEFNTLYHMHPLDPDFOIHQDKYKYOQFIYNNLSILHGTITOFVASFRTQIAGRY	420
Db	361	NRIAEFNTLYHMHPLDPDFOIHQDKYKYOQFIYNNLSILHGTITOFVASFRTQIAGRY	420
Qy	421	AGGRNPAPVQKVSQASIDQSRQMKYQSFNRYRKMFKPESFEELTGKEMSALEHL	480
Db	421	AGGRNPAPVQKVSQASIDQSRQMKYQSFNRYRKMFKPESFEELTGKEMSALEHL	480
Qy	481	YGDIDAVELEYPALVEKPRDPAIFQETWEVGAFFSLKGLMGVNTIGSPAWMKSTFGGEV	540
Db	481	YGDIDAVELEYPALVEKPRDPAIFQETWEVGAFFSLKGLMGVNTIGSPAWMKSTFGGEV	540
Qy	541	GFOIINTASIQSLICNNKGCPTFSVYDPDELLIKVTYINASSRSGLDINPTVLKER	600
Db	541	GFOIINTASIQSLICNNKGCPTFSVYDPDELLIKVTYINASSRSGLDINPTVLKER	600
Qy	601	STEL 604	
Db	601	STEL 604	

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RESULT 2
US-09-949-293-33
1 Sequence 33, Application US/099949293
2 Publication No. US2003008250A1
3 GENERAL INFORMATION:
4 APPLICANT: Thomann, Hans-Ulrich
5 APPLICANT: Wall, Kristian
6 APPLICANT: Fitzgerald, Michael
7 TITLE OF INVENTION: MUTATIONS OF THE CYCLOOXYGENASE-2 GENE
8 FILE REFERENCE: TECH01-07
9 CURRENT APPLICATION NUMBER: US/09/949,293
10 CURRENT FILING DATE: 2002-06-04
11 PRIOR APPLICATION NUMBER: 60/231,250
12 PRIOR FILING DATE: 2000-09-08
13 NUMBER OF SEQ ID NOS: 33
14 SOFTWARE: FastSBQ for Windows Version 4.0
15 SEQ ID NO 33
16 LENGTH: 604
17 TYPE: PRT
18 ORGANISM: Homo sapiens
19 US-09-949-293-33

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Query Match	100.0%;	Score 3237;	DB 10;	Length 604;
Best Local Similarity	100.0%;	Pred. No. 6.1e-313;		
Matches 604;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY		M L R A L L C G V A L S T A P C C S H P O N R G V C M S V G F O Y K D C T R T E Y E M N S T E F L	60
D b	1	M L R A L L C G V A L S T A P C C S H P O N R G V C M S V G F O Y K D C T R T E Y E M N S T E F L	60
OY		T R I K L F K P P N T V A H I L T H F K G F M V N V N I P F L A N I M S Y L T S R S H L I D S P T Y A D Y	120
D b	61	T R I K L F K P P N T V A H I L T H F K G F M V N V N I P F L A N I M S Y L T S R S H L I D S P T Y A D Y	120
OY		G Y K S W E A F S M L S Y T R A L P P V P D D C P T P L G V G K Q L P D S N E I V E K L L R R K F I P D B G S	180
D b	121	G Y K S W E A F S M L S Y T R A L P P V P D D C P T P L G V G K Q L P D S N E I V E K L L R R K F I P D B G S	180
OY		G Y K S W E A F S M L S Y T R A L P P V P D D C P T P L G V G K Q L P D S N E I V E K L L R R K F I P D B G S	180
D b	121	G Y K S W E A F S M L S Y T R A L P P V P D D C P T P L G V G K Q L P D S N E I V E K L L R R K F I P D B G S	180
OY		N M M F A P A Q H F T H O P F K T D H K R G A P T N L G H G V D L N H Y G E T L A R O K K L L F D G M K Y	240
D b	181	N M M F A P A Q H F T H O P F K T D H K R G A P T N L G H G V D L N H Y G E T L A R O K K L L F D G M K Y	240
OY		Q I I D E Y N P P T V K D Q A E M I Y P P Q V E H L R F A V G E V F L G E L M M Y A T I W L R E H N R V C D	300

Db	241	QIIDGEMVPRPVXDTQAMIVRPOVBEHLBRVAGVEVGLVPGMLMMVATIMLRHNRYCD	300
QY	301	VLKOEHPBWMGEOLFOISRLILIGETIKIVIEDYQIHSGYFKLKFPELLFNKQFOYO	360
Db	301	VLKOEHPBWMGEOLFQISRLILIGETIKIVIEDYQIHSGYFKLKFPELLFNKQFOYO	360
QY	361	NRIAEFNTLIVHMHPLBDFEQIHQOKNYOOQFINNSILHEGLTQFVESFTROJAGRY	420
Db	361	NRIAEFNTLIVHMHPLBDFEQIHQOKNYOOQFINNSILHEGLTQFVESFTROJAGRY	420
QY	421	AGGNVPRVAVOKVQASIDQSRQMKYQSFNEFKRKFMLKPYBSFELLTGEKMSALEAL	480
Db	421	AGGNVPRVAVOKVQASIDQSRQMKYQSFNEFKRKFMLKPYBSFELLTGEKMSALEAL	480
QY	481	YGDIDAVELYPALLVEKPRPDALFGETIWEVGAPELSLKGIMGNVITCSPAYMKPSTFGGEV	540
Db	481	YGDIDAVELYPALLVEKPRPDALFGETIWEVGAPELSLKGIMGNVITCSPAYMKPSTFGGEV	540
QY	541	GFOIINTASIOSLICNNVKGCFPTSFVSVPDPELLKTIVTINASSSRSGLDINPTVLLKER	600
Db	541	GFOIINTASIOSLICNNVKGCFPTSFVSVPDPELLKTIVTINASSSRSGLDINPTVLLKER	600
QY	601	STEL 604	
Db	601	STEL 604	

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RESULT 3
US-10-211-462-133
; Sequence 133, Application US/10211462
; Publication No. US2004003495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Nalasma
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-133

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Best Local Similarity	100.0%;	Pred. No. 6.1e-313;		
Matches 604;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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	Best Local	Similarity	100.0%	Pred. No. 6.1e-313	Mismatches 0	Indels 0
	Matches	604	Conservative	0	Gaps	0
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Db	1	MLARALLCAVALASHTANPCCSHPCQNGVCMVSGFDQKDCDCTRITGYGENCS7PEFL	60			
Qy	61	TRIKLFLKPEPTVHYILTFHFGFVNVNNIPEFLRANMSYVLTSSSHLIDSPPTNNADY	120			
Db	61	TRIKLFLKPEPTVHYILTFHFGFVNVNNIPEFLRANMSYVLTSSSHLIDSPPTNNADY	120			
Qy	121	GKRSWEAFENLSYVYRALPEVDDCETPLGVGVKKQOLPDSNEIVEKILLERKE1PDPQGS	180			
Db	121	GKRSWEAFENLSYVYRALPEVDDCETPLGVGVKKQOLPDSNEIVEKILLERKE1PDPQGS	180			

QY 181 NMFAFFAQTHTQFHTDHRKGPATNGLGHGVLDLNIH YGETTLARQRRLR.FKDGKMY 240
DB 181 NMFAFFAQTHTQFHTDHRKGPATNGLGHGVLDLNIH YGETTLARQRRLR.FKDGKMY 240
QY 241 QIIDGEMPTVKTQDAEMITPPOVBEHLRFVAVGVEGLVPGLMVYATIMLRHNRCVD 300
DB 241 QIIDGEMPTVKTQDAEMITPPOVBEHLRFVAVGVEGLVPGLMVYATIMLRHNRCVD 300
QY 301 VLKQHPHPEWDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKFPELLEFNKQFOYQ 360
DB 301 VLKQHPHPEWDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKFPELLEFNKQFOYQ 360
QY 361 NR1AAEFNTLYHMHLLPDTFOIHDQKYNVQOPIYNNLSILBHGITQFVESFTROIAGRV 420
DB 361 NR1AAEFNTLYHMHLLPDTFOIHDQKYNVQOPIYNNLSILBHGITQFVESFTROIAGRV 420
QY 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNYRKRKFMKPYESFEELTGEKEMSALEAL 480
DB 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNYRKRKFMKPYESFEELTGEKEMSALEAL 480
QY 481 YGDIIDAVELYPALLVEKRPDAIFGETMVEVGAPEFSLKGLMGVNICSPAYMKPSTFGEV 540
DB 481 YGDIIDAVELYPALLVEKRPDAIFGETMVEVGAPEFSLKGLMGVNICSPAYMKPSTFGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELIKYTTINASSRSGLDINPTVLLKER 600
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QY 601 STEL 604
DB 601 STEL 604

RESULT 4
US-10-170-385-237
; Sequence 237, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 53268200100
; CURRENT APPLICATION NUMBER: US/10170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-237

Query Match 100.0%; Score 3237; DB 12; Length 604;
Best Local Similarity 100.0%; Pred. No. 6.1e-313;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLARALLCAVALASHTANPCSHPCNRCVCMVSGVDQYKCDCTRTGFGENCSTPEFL 60
DB 1 MLARALLCAVALASHTANPCSHPCNRCVCMVSGVDQYKCDCTRTGFGENCSTPEFL 60

QY 61 TRIKLFLKPTNTVYHILTHFGFMNVYNNI PELNATMSVYLTSRSHLIDSPPTYNADY 120
DB 61 TRIKLFLKPTNTVYHILTHFGFMNVYNNI PELNATMSVYLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWAEPNSLSYTRALPVPDDCPTPLGVYKQKQLDPSNIEVKLLLRREFIDPQOS 180
DB 121 GYKSWAEPNSLSYTRALPVPDDCPTPLGVYKQKQLDPSNIEVKLLLRREFIDPQOS 180
QY 181 NMFAFFAQTHTQFHTDHRKGPATNGLGHGVLDLNIH YGETTLARQRRLR.FKDGKMY 240
DB 181 NMFAFFAQTHTQFHTDHRKGPATNGLGHGVLDLNIH YGETTLARQRRLR.FKDGKMY 240
QY 241 QIIDGEMPTVKTQDAEMITPPOVBEHLRFVAVGVEGLVPGLMVYATIMLRHNRCVD 300
DB 241 QIIDGEMPTVKTQDAEMITPPOVBEHLRFVAVGVEGLVPGLMVYATIMLRHNRCVD 300
QY 301 VLKQHPHPEWDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKFPELLEFNKQFOYQ 360
DB 301 VLKQHPHPEWDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKFPELLEFNKQFOYQ 360
QY 361 NR1AAEFNTLYHMHLLPDTFOIHDQKYNVQOPIYNNLSILBHGITQFVESFTROIAGRV 420
DB 361 NR1AAEFNTLYHMHLLPDTFOIHDQKYNVQOPIYNNLSILBHGITQFVESFTROIAGRV 420
QY 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNYRKRKFMKPYESFEELTGEKEMSALEAL 480
DB 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNYRKRKFMKPYESFEELTGEKEMSALEAL 480
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QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELIKYTTINASSRSGLDINPTVLLKER 600
DB 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELIKYTTINASSRSGLDINPTVLLKER 600
QY 601 STEL 604
DB 601 STEL 604

RESULT 5
US-10-027-961A-18
; Sequence 18, Application US/10027961A
; Publication No. US20030032789A1
; GENERAL INFORMATION:
; APPLICANT: MANCINI, JOSEPH A.
; APPLICANT: O'NEILL, GARY P.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; FILE REFERENCE: 19029PCADA
; CURRENT APPLICATION NUMBER: US/10/027, 961A
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/599,781
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 08/930,589
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: PCT/CA94/00501
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/084,033
; PRIOR FILING DATE: 1993-09-27
; PRIOR APPLICATION NUMBER: 08/064,271
; PRIOR FILING DATE: 1993-05-06
; PRIOR APPLICATION NUMBER: 07/994,760
; PRIOR FILING DATE: 1992-12-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Human
US-10-027-961A-18

Query Match 100.0%; Score 3237; DB 14; Length 604;
 Best Local Similarity 100.0%; Pred. No. 6.1e-313;
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MLARALLCAVLAISHANPCSSHPCCNRGCMVGVFGYKCDCTRTGFGYENCSSTPEFL 60
DB 1 MLARALLCAVLAISHANPCSSHPCCNRGCMVGVFGYKCDCTRTGFGYENCSSTPEFL 60
OY 61 TRIKLFKPTNTVHYILLTHEKGFNNVNNIPELRNAIMSVYLSRSHLIDSPPTVADY 120
DB 61 TRIKLFKPTNTVHYILLTHEKGFNNVNNIPELRNAIMSVYLSRSHLIDSPPTVADY 120
OY 121 GYKSWFAFNSISYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRKKFLPDPQGS 180
DB 121 GYKSWFAFNSISYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRKKFLPDPQGS 180
OY 121 GYKSWFAFNSISYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRKKFLPDPQGS 180
DB 121 GYKSWFAFNSISYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRKKFLPDPQGS 180
OY 181 NMFAFPAQHPTTHQFPTDKHGRPAFTNGLGHVLDNIYGETLARQRKLLFDGKKMY 240
DB 181 NMFAFPAQHPTTHQFPTDKHGRPAFTNGLGHVLDNIYGETLARQRKLLFDGKKMY 240
OY 241 QIIDGEMYPPTVKDQAEMIVPQVBEHLRPAVGQEVGLVPGIMVATIMLRHNRYCD 300
DB 241 QIIDGEMYPPTVKDQAEMIVPQVBEHLRPAVGQEVGLVPGIMVATIMLRHNRYCD 300
OY 301 VLKQHPHWSGBOUFGTSRLILIGETIKIVIEDVYQHLSGVHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQHPHWSGBOUFGTSRLILIGETIKIVIEDVYQHLSGVHFKLKPDELLFNKQFOYQ 360
OY 361 NR1AAEFNTLHYMHPLPDTFOIHQKXNYOQFIYNNLSILHEG1TQVESPTRQIARV 420
DB 361 NR1AAEFNTLHYMHPLPDTFOIHQKXNYOQFIYNNLSILHEG1TQVESPTRQIARV 420
OY 421 AGGRNVPVAVQKVSQASIDQSRQMKYQSFNERYKRPMLKPYHSFELTGEKEMSEALAL 480
DB 421 AGGRNVPVAVQKVSQASIDQSRQMKYQSFNERYKRPMLKPYHSFELTGEKEMSEALAL 480
OY 481 YGDDDAVELYPLALVEKRPDAIFGETWVEVGAAPSLKGMGNVCSPAYMKPSTFGGEV 540
DB 481 YGDDDAVELYPLALVEKRPDAIFGETWVEVGAAPSLKGMGNVCSPAYMKPSTFGGEV 540
OY 541 GFQIINTASIOGLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPVLKER 600
DB 541 GFQIINTASIOGLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPVLKER 600
OY 601 STEL 604
DB 601 STEL 604

```

RESULT 6
 US-10-021-660-109
 ; Sequence 109, Application US/10021660
 ; Publication No. US20030152926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Glyme, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: EOS Biotechnology, Inc.
 ; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,
 ; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
 ; TITLE OF INVENTION: Modulators
 ; FILE REFERENCE: 018501-000710US
 ; CURRENT APPLICATION NUMBER: US/10/021,660
 ; CURRENT FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: US/09/784,356
 ; PRIOR FILING DATE: 2001-02-14
 ; PRIOR APPLICATION NUMBER: US 09/637,977
 ; PRIOR FILING DATE: 2000-08-11
 ; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 109
 ; LENGTH: 604
 ; TYPE: PRT

ORGANISM: Homo sapiens
 US-10-021-660-109

Query Match 100.0%; Score 3237; DB 14; Length 604;
 Best Local Similarity 100.0%; Pred. No. 6.1e-313;
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MLARALLCAVLAISHANPCSSHPCCNRGCMVGVFGYKCDCTRTGFGYENCSSTPEFL 60
DB 1 MLARALLCAVLAISHANPCSSHPCCNRGCMVGVFGYKCDCTRTGFGYENCSSTPEFL 60
OY 61 TRIKLFKPTNTVHYILLTHEKGFNNVNNIPELRNAIMSVYLSRSHLIDSPPTVADY 120
DB 61 TRIKLFKPTNTVHYILLTHEKGFNNVNNIPELRNAIMSVYLSRSHLIDSPPTVADY 120
OY 121 GYKSWFAFNSISYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRKKFLPDPQGS 180
DB 121 GYKSWFAFNSISYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRKKFLPDPQGS 180
OY 121 GYKSWFAFNSISYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRKKFLPDPQGS 180
DB 121 GYKSWFAFNSISYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRKKFLPDPQGS 180
OY 181 NMFAFPAQHPTTHQFPTDKHGRPAFTNGLGHVLDNIYGETLARQRKLLFDGKKMY 240
DB 181 NMFAFPAQHPTTHQFPTDKHGRPAFTNGLGHVLDNIYGETLARQRKLLFDGKKMY 240
OY 241 QIIDGEMYPPTVKDQAEMIVPQVBEHLRPAVGQEVGLVPGIMVATIMLRHNRYCD 300
DB 241 QIIDGEMYPPTVKDQAEMIVPQVBEHLRPAVGQEVGLVPGIMVATIMLRHNRYCD 300
OY 301 VLKQHPHWSGBOUFGTSRLILIGETIKIVIEDVYQHLSGVHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQHPHWSGBOUFGTSRLILIGETIKIVIEDVYQHLSGVHFKLKPDELLFNKQFOYQ 360
OY 361 NR1AAEFNTLHYMHPLPDTFOIHQKXNYOQFIYNNLSILHEG1TQVESPTRQIARV 420
DB 361 NR1AAEFNTLHYMHPLPDTFOIHQKXNYOQFIYNNLSILHEG1TQVESPTRQIARV 420
OY 421 AGGRNVPVAVQKVSQASIDQSRQMKYQSFNERYKRPMLKPYHSFELTGEKEMSEALAL 480
DB 421 AGGRNVPVAVQKVSQASIDQSRQMKYQSFNERYKRPMLKPYHSFELTGEKEMSEALAL 480
OY 481 YGDDDAVELYPLALVEKRPDAIFGETWVEVGAAPSLKGMGNVCSPAYMKPSTFGGEV 540
DB 481 YGDDDAVELYPLALVEKRPDAIFGETWVEVGAAPSLKGMGNVCSPAYMKPSTFGGEV 540
OY 541 GFQIINTASIOGLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPVLKER 600
DB 541 GFQIINTASIOGLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPVLKER 600
OY 601 STEL 604
DB 601 STEL 604

```

RESULT 7
 US-10-260-937-22
 ; Sequence 22, Application US/10260937
 ; Publication No. US20030220306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Simmons, Daniel
 ; APPLICANT: Chandrasekharan, N. Vishvanath
 ; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
 ; TITLE OF INVENTION: METHODS OF USE
 ; FILE REFERENCE: 07913-007001
 ; CURRENT APPLICATION NUMBER: US/10/260,937
 ; CURRENT FILING DATE: 2002-09-28
 ; PRIOR APPLICATION NUMBER: US 60/326,133
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: US 60/373,225
 ; PRIOR FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: US 60/373,661
 ; PRIOR FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: US 60/411,575
 ; PRIOR FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 89

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 22
 LENGTH: 604
 TYPE: PR
 ORGANISM: Homo sapiens
 US-10-260-937-22

Query Match 100.0%; Score 3237; DB 15; Length 604;
 Best Local Similarity 100.0%; Pred. No. 6,1e-313;
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MABALLCAVALALSHSTANPCSHPCQNGVCMGVGFDDYKDCDCTRTGYGNCSTPEL 60
DB 1 MABALLCAVALALSHSTANPCSHPCQNGVCMGVGFDDYKDCDCTRTGYGNCSTPEL 60
QY 61 TRIKLEKPTVTYVYIITHEKGFNNVNNIPELRNAMSYYLTSSSHLIDSPPTYNADY 120
DB 61 TRIKLEKPTVTYVYIITHEKGFNNVNNIPELRNAMSYYLTSSSHLIDSPPTYNADY 120
QY 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
QY 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
QY 181 NMMAFAFQHFTHQFETDHRKGPFTNGLGHVLDNIHYGETLARQRKRLFKDGKMKY 240
DB 181 NMMAFAFQHFTHQFETDHRKGPFTNGLGHVLDNIHYGETLARQRKRLFKDGKMKY 240
QY 241 QIIDEMYPPTVKDQOAMITPPQVPEHLRPAVGOEFGVLVGLMMYATIMLREHNRVCD 300
DB 241 QIIDEMYPPTVKDQOAMITPPQVPEHLRPAVGOEFGVLVGLMMYATIMLREHNRVCD 300
QY 301 VLKQHPHWDQOLFQTSRLIIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQHPHWDQOLFQTSRLIIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
QY 361 NRIAEFNTLYHMHLPDPTFOIHDQKNYQOFTYNNLSILHEGITTQVESTTRQIARV 420
DB 361 NRIAEFNTLYHMHLPDPTFOIHDQKNYQOFTYNNLSILHEGITTQVESTTRQIARV 420
QY 421 AGGRNVPPAVQKVSQASIDSRQMKYOSFNEYRKFPMKPYBSPELTGEXKMSALEL 480
DB 421 AGGRNVPPAVQKVSQASIDSRQMKYOSFNEYRKFPMKPYBSPELTGEXKMSALEL 480
QY 481 YGIDDAVELYPALIVEKRPDAIFGETWVEVGAPELSKLGNGVICSAPYMKPSTFGGAV 540
DB 481 YGIDDAVELYPALIVEKRPDAIFGETWVEVGAPELSKLGNGVICSAPYMKPSTFGGAV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELIKVTITNASSRSGLDIDNPVLKEX 600
DB 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELIKVTITNASSRSGLDIDNPVLKEX 600
QY 601 STEL 604
DB 601 STEL 604

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RESULT 8
 US-10-295-027-32
 Sequence 32, Application US/10295027
 Publication No. US2003023250A1
 GENERAL INFORMATION:
 APPLICANT: Afar, Daniel
 APPLICANT: Aziz, Natasha
 APPLICANT: Ginsberg, Wendy M.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Glynn, Richard
 APPLICANT: Hevezi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: Eos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 TITLE OF INVENTION: Methods of Screening for Modulators of Cancer

FILE REFERENCE: 018501-012500US
 CURRENT APPLICATION NUMBER: US/10/295, 027
 PRIOR FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663, 733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350, 666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335, 394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332, 464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334, 393
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: US 60/340, 376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347, 211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347, 349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355, 250
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: US 60/356, 714
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 32
 LENGTH: 604
 TYPE: PR
 ORGANISM: Homo sapiens
 US-10-295-027-32

Query Match 100.0%; Score 3237; DB 15; Length 604;
 Best Local Similarity 100.0%; Pred. No. 6,1e-313;
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MABALLCAVALALSHSTANPCSHPCQNGVCMGVGFDDYKDCDCTRTGYGNCSTPEL 60
DB 1 MABALLCAVALALSHSTANPCSHPCQNGVCMGVGFDDYKDCDCTRTGYGNCSTPEL 60
QY 61 TRIKLEKPTVTYVYIITHEKGFNNVNNIPELRNAMSYYLTSSSHLIDSPPTYNADY 120
DB 61 TRIKLEKPTVTYVYIITHEKGFNNVNNIPELRNAMSYYLTSSSHLIDSPPTYNADY 120
QY 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
QY 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
QY 181 NMMAFAFQHFTHQFETDHRKGPFTNGLGHVLDNIHYGETLARQRKRLFKDGKMKY 240
DB 181 NMMAFAFQHFTHQFETDHRKGPFTNGLGHVLDNIHYGETLARQRKRLFKDGKMKY 240
QY 241 QIIDEMYPPTVKDQOAMITPPQVPEHLRPAVGOEFGVLVGLMMYATIMLREHNRVCD 300
DB 241 QIIDEMYPPTVKDQOAMITPPQVPEHLRPAVGOEFGVLVGLMMYATIMLREHNRVCD 300
QY 301 VLKQHPHWDQOLFQTSRLIIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQHPHWDQOLFQTSRLIIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
QY 361 NRIAEFNTLYHMHLPDPTFOIHDQKNYQOFTYNNLSILHEGITTQVESTTRQIARV 420
DB 361 NRIAEFNTLYHMHLPDPTFOIHDQKNYQOFTYNNLSILHEGITTQVESTTRQIARV 420
QY 421 AGGRNVPPAVQKVSQASIDSRQMKYOSFNEYRKFPMKPYBSPELTGEXKMSALEL 480
DB 421 AGGRNVPPAVQKVSQASIDSRQMKYOSFNEYRKFPMKPYBSPELTGEXKMSALEL 480
QY 481 YGIDDAVELYPALIVEKRPDAIFGETWVEVGAPELSKLGNGVICSAPYMKPSTFGGAV 540
DB 481 YGIDDAVELYPALIVEKRPDAIFGETWVEVGAPELSKLGNGVICSAPYMKPSTFGGAV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELIKVTITNASSRSGLDIDNPVLKEX 600

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DB      541 GFOINTASISQILCNVKGCPFTSPVDPBELIKVTITNASSRSGLDINPTVLKER 600
QY      601 STEL 604
DB      601 STEL 604

RESULT 9
US-10-373-801-30
; Sequence 30, Application US/10373801
; Publication No. US20040005644A1
; GENERAL INFORMATION:
; APPLICANT: Vialat Pharmaceutical (USA)
; TITLE OF INVENTION: Method and composition for detection and treatment of breast can
; FILE REFERENCE: 12399.00
; CURRENT APPLICATION NUMBER: US/10/373,801
; CURRENT FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 30
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-373-801-30

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```

Query Match      100.0%; Score 3237; DB 15; Length 604;
Best Local Similarity 100.0%; Pred. No. 6.1e-313;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 MLARALLICAVLALSHSTANPCSCSPQNGVCMVSGVDFDYKCDCTRTGFGNGCSTPEEL 60
DB      1 MLARALLICAVLALSHSTANPCSCSPQNGVCMVSGVDFDYKCDCTRTGFGNGCSTPEEL 60
QY      61 TRIKLFLKPTPTVNHILTHFGKGFVNVNIPILRAIMSIVLTSSHLIDSPPTYNADY 120
DB      61 TRIKLFLKPTPTVNHILTHFGKGFVNVNIPILRAIMSIVLTSSHLIDSPPTYNADY 120
QY      121 GYKSWAFNSLSTYTRALPVPVDDCPTPLGVKGGKOLPDSNETIVEKLLLRKFIIPDQGS 180
DB      121 GYKSWAFNSLSTYTRALPVPVDDCPTPLGVKGGKOLPDSNETIVEKLLLRKFIIPDQGS 180
QY      121 GYKSWAFNSLSTYTRALPVPVDDCPTPLGVKGGKOLPDSNETIVEKLLLRKFIIPDQGS 180
DB      121 GYKSWAFNSLSTYTRALPVPVDDCPTPLGVKGGKOLPDSNETIVEKLLLRKFIIPDQGS 180
QY      181 NMMAFAFHQFTHOFKTDHKGPAFTNGIGHGVNDINHLYGETTLAROKRLRFKDGKMY 240
DB      181 NMMAFAFHQFTHOFKTDHKGPAFTNGIGHGVNDINHLYGETTLAROKRLRFKDGKMY 240
QY      241 QIIDGMYPTVYKDTQAEIMYPPQVPEHLRFVAGQEVFGLVPGIMMYATTIMLRHNRYCD 300
DB      241 QIIDGMYPTVYKDTQAEIMYPPQVPEHLRFVAGQEVFGLVPGIMMYATTIMLRHNRYCD 300
QY      301 VLKQHPHMGDQOLFQTSRLILIGETIKIVIEDYVGHLSGYHFKLKFDELLFNKOFOYQ 360
DB      301 VLKQHPHMGDQOLFQTSRLILIGETIKIVIEDYVGHLSGYHFKLKFDELLFNKOFOYQ 360
QY      361 NR1AAEFNTLYMHPLLPDTFOIHDQKYNVOQFTYNNSSILLEGITQFVESFTROJAGRY 420
DB      361 NR1AAEFNTLYMHPLLPDTFOIHDQKYNVOQFTYNNSSILLEGITQFVESFTROJAGRY 420
QY      421 AGGRNVPVAVOKVQASIDOSRQMKYQSFNEYKRRLKPYSEFEEITGEKEMASALEAL 480
DB      421 AGGRNVPVAVOKVQASIDOSRQMKYQSFNEYKRRLKPYSEFEEITGEKEMASALEAL 480
QY      481 YGDIIDAVELYPALLVKPRPDALFGETWVEVGAFFSLKGLMGVNICSPAWMKSTEGEV 540
DB      481 YGDIIDAVELYPALLVKPRPDALFGETWVEVGAFFSLKGLMGVNICSPAWMKSTEGEV 540
QY      541 GFOINTASISQILCNVKGCPFTSPVDPBELIKVTITNASSRSGLDINPTVLKER 600
DB      541 GFOINTASISQILCNVKGCPFTSPVDPBELIKVTITNASSRSGLDINPTVLKER 600

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RESULT 10
US-10-260-937-27
; Sequence 27, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishwanath
; TITLE OF INVENTION: NOVEL CYCLOXYGENASE VARIANTS AND
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 27
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-260-937-27

```

```

Query Match      91.8%; Score 2971; DB 15; Length 604;
Best Local Similarity 89.9%; Pred. No. 1.9e-286;
Matches 543; Conservative 35; Mismatches 26; Indels 0; Gaps 0;

```

```

QY      1 MLARALLICAVLALSHSTANPCSCSPQNGVCMVSGVDFDYKCDCTRTGFGNGCSTPEEL 60
DB      1 MLARALLICAVLALSHSTANPCSCSPQNGVCMVSGVDFDYKCDCTRTGFGNGCSTPEEL 60
QY      61 TRIKLFLKPTPTVNHILTHFGKGFVNVNIPILRAIMSIVLTSSHLIDSPPTYNADY 120
DB      61 TRIKLFLKPTPTVNHILTHFGKGFVNVNIPILRAIMSIVLTSSHLIDSPPTYNADY 120
QY      121 GYKSWAFNSLSTYTRALPVPVDDCPTPLGVKGGKOLPDSNETIVEKLLLRKFIIPDQGS 180
DB      121 GYKSWAFNSLSTYTRALPVPVDDCPTPLGVKGGKOLPDSNETIVEKLLLRKFIIPDQGS 180
QY      121 GYKSWAFNSLSTYTRALPVPVDDCPTPLGVKGGKOLPDSNETIVEKLLLRKFIIPDQGS 180
DB      121 GYKSWAFNSLSTYTRALPVPVDDCPTPLGVKGGKOLPDSNETIVEKLLLRKFIIPDQGS 180
QY      181 NMMAFAFHQFTHOFKTDHKGPAFTNGIGHGVNDINHLYGETTLAROKRLRFKDGKMY 240
DB      181 NMMAFAFHQFTHOFKTDHKGPAFTNGIGHGVNDINHLYGETTLAROKRLRFKDGKMY 240
QY      241 QIIDGMYPTVYKDTQAEIMYPPQVPEHLRFVAGQEVFGLVPGIMMYATTIMLRHNRYCD 300
DB      241 QIIDGMYPTVYKDTQAEIMYPPQVPEHLRFVAGQEVFGLVPGIMMYATTIMLRHNRYCD 300
QY      301 VLKQHPHMGDQOLFQTSRLILIGETIKIVIEDYVGHLSGYHFKLKFDELLFNKOFOYQ 360
DB      301 VLKQHPHMGDQOLFQTSRLILIGETIKIVIEDYVGHLSGYHFKLKFDELLFNKOFOYQ 360
QY      361 NR1AAEFNTLYMHPLLPDTFOIHDQKYNVOQFTYNNSSILLEGITQFVESFTROJAGRY 420
DB      361 NR1AAEFNTLYMHPLLPDTFOIHDQKYNVOQFTYNNSSILLEGITQFVESFTROJAGRY 420
QY      421 AGGRNVPVAVOKVQASIDOSRQMKYQSFNEYKRRLKPYSEFEEITGEKEMASALEAL 480
DB      421 AGGRNVPVAVOKVQASIDOSRQMKYQSFNEYKRRLKPYSEFEEITGEKEMASALEAL 480
QY      481 YGDIIDAVELYPALLVKPRPDALFGETWVEVGAFFSLKGLMGVNICSPAWMKSTEGEV 540
DB      481 YGDIIDAVELYPALLVKPRPDALFGETWVEVGAFFSLKGLMGVNICSPAWMKSTEGEV 540
QY      541 GFOINTASISQILCNVKGCPFTSPVDPBELIKVTITNASSRSGLDINPTVLKER 600
DB      541 GFOINTASISQILCNVKGCPFTSPVDPBELIKVTITNASSRSGLDINPTVLKER 600

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QY 601 STEL 604
 Db 601 STEL 604

RESULT 11
 US-09-919-060-5
 ; Sequence 5, Application US/09919060
 ; Patent No. US20020064845A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wisniewski, Nancy
 ; APPLICANT: Brandt, Kevin S.
 ; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
 ; FILE REFERENCE: AD-1
 ; CURRENT APPLICATION NUMBER: US/09/919,060
 ; PRIOR FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: 60/224,486
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 604
 ; TYPE: PRT
 ; ORGANISM: Canis familiaris
 US-09-919-060-5

Query Match 91.7%; Score 2967; DB 9; Length 604;
 Best Local Similarity 90.1%; Pred. No. 4,8e-286;
 Matches 544; Conservative 30; Mismatches 30; Indels 0; Gaps 0;

QY 1 MLARALLICAVIALSHITANPCCSHPCQNRGVCMGVGFPOYKDCDCTRTGFGYGCSTPEFL 60
 1 MLARALVLCALAVVRAANPCCSHPCQNRGVCMGVGFPOYKDCDCTRTGFGYGCSTPEFL 60
 Db 61 TRIKFLKPTPTNYHYIITTHFGKFNWVNNIPLRLNATMSYVLSRSHLIDSPPTYNADY 120
 61 TRIKFLKPTPTNYHYIITTHFGKFNWVNNIPLRLNATMSYVLSRSHLIDSPPTYNADY 120
 QY 121 GYKSWAESNLSYSTRALPVPYDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180
 121 GYKSWAESNLSYSTRALPVPYDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180
 Db 121 GYKSWAESNLSYSTRALPVPYDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180
 121 GYKSWAESNLSYSTRALPVPYDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180
 QY 181 NMMEFAFQHFTHQFFKTDHKGPAFTNGLGHGVDLNIYGEETLARKOKLFLFKDGKKKY 240
 181 NMMEFAFQHFTHQFFKTDHKGPAFTNGLGHGVDLNIYGEETLARKOKLFLFKDGKKKY 240
 Db 181 NMMEFAFQHFTHQFFKTDHKGPAFTNGLGHGVDLNIYGEETLARKOKLFLFKDGKKKY 240
 181 NMMEFAFQHFTHQFFKTDHKGPAFTNGLGHGVDLNIYGEETLARKOKLFLFKDGKKKY 240
 QY 241 QIINGEMVPTVKQTQAMETYPQVPEHLRPAVGQEVFGLVGLMMYATTMLREHNRVCD 300
 241 QIINGEMVPTVKQTQAMETYPQVPEHLRPAVGQEVFGLVGLMMYATTMLREHNRVCD 300
 Db 241 QIINGEMVPTVKQTQAMETYPQVPEHLRPAVGQEVFGLVGLMMYATTMLREHNRVCD 300
 241 QIINGEMVPTVKQTQAMETYPQVPEHLRPAVGQEVFGLVGLMMYATTMLREHNRVCD 300
 QY 301 VLKQHEPMDERLFOFTRSLILIGETIKIVIEDVYQHLSGYHFKLKPDPBELLPKOPQYQ 360
 301 VLKQHEPMDERLFOFTRSLILIGETIKIVIEDVYQHLSGYHFKLKPDPBELLPKOPQYQ 360
 Db 301 VLKQHEPMDERLFOFTRSLILIGETIKIVIEDVYQHLSGYHFKLKPDPBELLPKOPQYQ 360
 301 VLKQHEPMDERLFOFTRSLILIGETIKIVIEDVYQHLSGYHFKLKPDPBELLPKOPQYQ 360
 QY 361 NRIAAEFTLYHMHPLLPDTFQIDHOKXNYQOFTYNNLSILHEGITQFVESFTQIAGRV 420
 361 NRIAAEFTLYHMHPLLPDTFQIDHOKXNYQOFTYNNLSILHEGITQFVESFTQIAGRV 420
 Db 361 NRIAAEFTLYHMHPLLPDTFQIDHOKXNYQOFTYNNLSILHEGITQFVESFTQIAGRV 420
 361 NRIAAEFTLYHMHPLLPDTFQIDHOKXNYQOFTYNNLSILHEGITQFVESFTQIAGRV 420
 QY 421 AGGNVPPAYOKVSQASIDOSRQMKYOSFNEYRKRFLMKRYESBEELTGEKEMGALEAL 480
 421 AGGNVPPAYOKVSQASIDOSRQMKYOSFNEYRKRFLMKRYESBEELTGEKEMGALEAL 480
 Db 421 AGGNVPPAYOKVSQASIDOSRQMKYOSFNEYRKRFLMKRYESBEELTGEKEMGALEAL 480
 421 AGGNVPPAYOKVSQASIDOSRQMKYOSFNEYRKRFLMKRYESBEELTGEKEMGALEAL 480
 QY 481 YGDIIDAVELYPALIVEKRPDAIFGETMVEVGAFPSLKGIMGNVICSAPYKPSPTFGGEV 540
 481 YGDIIDAVELYPALIVEKRPDAIFGETMVEVGAFPSLKGIMGNVICSAPYKPSPTFGGEV 540
 Db 481 YGDIIDAVELYPALIVEKRPDAIFGETMVEVGAFPSLKGIMGNVICSAPYKPSPTFGGEV 540
 481 YGDIIDAVELYPALIVEKRPDAIFGETMVEVGAFPSLKGIMGNVICSAPYKPSPTFGGEV 540
 QY 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELTKYVTINASSRSGLDINPTVLKER 600
 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELTKYVTINASSRSGLDINPTVLKER 600
 Db 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELTKYVTINASSRSGLDINPTVLKER 600
 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELTKYVTINASSRSGLDINPTVLKER 600
 QY 601 STEL 604
 601 STEL 604

Db 601 STEL 604

RESULT 12
 US-09-949-293-30
 ; Sequence 30, Application US/09949293
 ; Publication No. US20030082550A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thoenen, Hans-Ulrich
 ; APPLICANT: Wall, Kristian
 ; APPLICANT: Fitzgerald, Michael
 ; TITLE OF INVENTION: MUTATIONS OF THE CYCLOOXYGENASE-2 GENE
 ; FILE REFERENCE: TECH01-07
 ; CURRENT APPLICATION NUMBER: US/09/949,293
 ; PRIOR FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: 60/231,250
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 30
 ; LENGTH: 604
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-949-293-30

Query Match 90.8%; Score 2938; DB 10; Length 604;
 Best Local Similarity 88.9%; Pred. No. 3.7e-283;
 Matches 537; Conservative 35; Mismatches 32; Indels 0; Gaps 0;

QY 1 MLARALLICAVIALSHITANPCCSHPCQNRGVCMGVGFPOYKDCDCTRTGFGYGCSTPEFL 60
 1 MLARALVLCALAVVRAANPCCSHPCQNRGVCMGVGFPOYKDCDCTRTGFGYGCSTPEFL 60
 Db 61 TRIKFLKPTPTNYHYIITTHFGKFNWVNNIPLRLNATMSYVLSRSHLIDSPPTYNADY 120
 61 TRIKFLKPTPTNYHYIITTHFGKFNWVNNIPLRLNATMSYVLSRSHLIDSPPTYNADY 120
 QY 121 GYKSWAESNLSYSTRALPVPYDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180
 121 GYKSWAESNLSYSTRALPVPYDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180
 Db 121 GYKSWAESNLSYSTRALPVPYDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180
 121 GYKSWAESNLSYSTRALPVPYDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180
 QY 181 NMMEFAFQHFTHQFFKTDHKGPAFTNGLGHGVDLNIYGEETLARKOKLFLFKDGKKKY 240
 181 NMMEFAFQHFTHQFFKTDHKGPAFTNGLGHGVDLNIYGEETLARKOKLFLFKDGKKKY 240
 Db 181 NMMEFAFQHFTHQFFKTDHKGPAFTNGLGHGVDLNIYGEETLARKOKLFLFKDGKKKY 240
 181 NMMEFAFQHFTHQFFKTDHKGPAFTNGLGHGVDLNIYGEETLARKOKLFLFKDGKKKY 240
 QY 241 QIINGEMVPTVKQTQAMETYPQVPEHLRPAVGQEVFGLVGLMMYATTMLREHNRVCD 300
 241 QIINGEMVPTVKQTQAMETYPQVPEHLRPAVGQEVFGLVGLMMYATTMLREHNRVCD 300
 Db 241 QIINGEMVPTVKQTQAMETYPQVPEHLRPAVGQEVFGLVGLMMYATTMLREHNRVCD 300
 241 QIINGEMVPTVKQTQAMETYPQVPEHLRPAVGQEVFGLVGLMMYATTMLREHNRVCD 300
 QY 301 VLKQHEPMDERLFOFTRSLILIGETIKIVIEDVYQHLSGYHFKLKPDPBELLPKOPQYQ 360
 301 VLKQHEPMDERLFOFTRSLILIGETIKIVIEDVYQHLSGYHFKLKPDPBELLPKOPQYQ 360
 Db 301 VLKQHEPMDERLFOFTRSLILIGETIKIVIEDVYQHLSGYHFKLKPDPBELLPKOPQYQ 360
 301 VLKQHEPMDERLFOFTRSLILIGETIKIVIEDVYQHLSGYHFKLKPDPBELLPKOPQYQ 360
 QY 361 NRIAAEFTLYHMHPLLPDTFQIDHOKXNYQOFTYNNLSILHEGITQFVESFTQIAGRV 420
 361 NRIAAEFTLYHMHPLLPDTFQIDHOKXNYQOFTYNNLSILHEGITQFVESFTQIAGRV 420
 Db 361 NRIAAEFTLYHMHPLLPDTFQIDHOKXNYQOFTYNNLSILHEGITQFVESFTQIAGRV 420
 361 NRIAAEFTLYHMHPLLPDTFQIDHOKXNYQOFTYNNLSILHEGITQFVESFTQIAGRV 420
 QY 421 AGGNVPPAYOKVSQASIDOSRQMKYOSFNEYRKRFLMKRYESBEELTGEKEMGALEAL 480
 421 AGGNVPPAYOKVSQASIDOSRQMKYOSFNEYRKRFLMKRYESBEELTGEKEMGALEAL 480
 Db 421 AGGNVPPAYOKVSQASIDOSRQMKYOSFNEYRKRFLMKRYESBEELTGEKEMGALEAL 480
 421 AGGNVPPAYOKVSQASIDOSRQMKYOSFNEYRKRFLMKRYESBEELTGEKEMGALEAL 480
 QY 481 YGDIIDAVELYPALIVEKRPDAIFGETMVEVGAFPSLKGIMGNVICSAPYKPSPTFGGEV 540
 481 YGDIIDAVELYPALIVEKRPDAIFGETMVEVGAFPSLKGIMGNVICSAPYKPSPTFGGEV 540
 Db 481 YGDIIDAVELYPALIVEKRPDAIFGETMVEVGAFPSLKGIMGNVICSAPYKPSPTFGGEV 540
 481 YGDIIDAVELYPALIVEKRPDAIFGETMVEVGAFPSLKGIMGNVICSAPYKPSPTFGGEV 540
 QY 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELTKYVTINASSRSGLDINPTVLKER 600
 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELTKYVTINASSRSGLDINPTVLKER 600
 Db 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELTKYVTINASSRSGLDINPTVLKER 600
 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELTKYVTINASSRSGLDINPTVLKER 600
 QY 601 STEL 604
 601 STEL 604

```

1      RESULT 13
2      US-10-260-937-26
3      : Sequence 26. Application US/10260937
4      : Publication NO. US20030220306A1
5      : GENERAL INFORMATION:
6      : APPLICANT: Simmons, Daniel
7      : APPLICANT: Chandrasekharan, N. Vishvanath
8      : TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
9      : TITLE OF INVENTION: METHODS OF USE
10     : FILE REFERENCE: 07913-007001
11     : CURRENT APPLICATION NUMBER: US/10/260,937
12     : CURRENT FILING DATE: 2002-09-28
13     : PRIOR APPLICATION NUMBER: US 60/326,133
14     : PRIOR FILING DATE: 2001-09-28
15     : PRIOR APPLICATION NUMBER: US 60/373,225
16     : PRIOR FILING DATE: 2002-04-15
17     : PRIOR APPLICATION NUMBER: US 60/373,661
18     : PRIOR FILING DATE: 2002-04-16
19     : PRIOR APPLICATION NUMBER: US 60/411,575
20     : PRIOR FILING DATE: 2002-09-16
21     : NUMBER OF SEQ ID NOS: 89
22     : SOFTWARE: FastSeq For Windows Version 4.0
23     : SEQ ID NO 26
24     : LENGTH: 604
25     : TYPE: PRT
26     : ORGANISM: Equus caballus
27     : US-10-260-937-26

```

QY	1	MLAALALLCAVALIASHTEHNPCCHSCQNRGCMGSGPFOYKODCRTCRTGVCNGCSTPEL	60
Db	1	MLARLLLCVALIASHAANPCCCSNPCQNRGCMGSGPFOYQDDCRTCRTGVCNGCSTPEL	60
QY	61	TRILFLKPEPTNTVAYILTHFGKFNNVANNIPELTNAIMSYLTSRSHLIDSPPTYNADY	120
Db	61	TRILFLKPEPTNTVAYILTHFGKGVANNIINSPPELTNAAIMKYLVSRSHLIESPPTYNQY	120
QY	121	GYSKWEAFNSLSSYTRALRPVYDPCPYLGVYKKQKQLPDSNEIYKLLIRKRFIDPQGS	180
Db	121	GYSKWEFSNSLSYTRALRPVADCGPTPMGVYKKELPDSKEIYKFLIRKRFIDPQGT	180
QY	181	NMMAFEPFOHETHOFEKTDHKRGPAFTNGLSGVQNLNIYEGTTAROKRLRFKQKKMY	240
Db	181	NMMAFEPFOHETHOFEKTDPKRGPAFTIGLGVQNLSHIYEGTTDRÖHKRLRFKQKKMY	240
QY	241	QIIDGEMRPVYKDTQOQAEIMYRPPQVPEHLRFVAGOEVLGVGLMMVATIMLRHNRYCD	300
Db	241	QIINSEVVRPYKDTQVEMIMYRPHIPEHLRFVAGOEVLGVGLMMVATIMLRHNRYCD	300
QY	301	VLKQHPHWDGDLFQTSRLITIGTTIKIVIEDYVQHLSGYHFKLKPEDELLPNKQFOYQ	360
Db	301	VLKQHPHWDDEHRLFQTSRLITIGETIKIVIEDYVQHLSGYHFKLKPEDELLPFNOQFOYQ	360
QY	361	NRIAAEENLIVHMHLLPDTFOIHOKNNYQOIFNNSSLIEHGLTQFPESTFROIAGV	420
Db	361	NRIAAEENLIVHMHLLPDTFOIDOBINFOQLNNSSLIEHGLTQFPESSRSOIAGV	420
QY	421	AGGRVAPVAVOKVASIDOSROMKYOSFNEKRRKFMKPYESPEELTGEKEMSALEAL	480
Db	421	AGGRVAPPAQKIAKASIDQSRKEMKYOSLNEKRRKFMFLPYKSPFELTGEKMAALEAL	480
QY	481	YGDIDAVELYPALIVKRPBDALFGEITWEGAPPSLKGLMGVIVICSPAIVKRPSTFGGEV	540
Db	481	YGDIDAMELYPALIVKRPBDALFGEITWELGAPPSLKGLGNPICSPEYKRPSTFGGEV	540
QY	541	GFOIINTASIOSLONNWKGGCFSTFSVPDELLIKVTINASSRSGLDINDIPVYLKKR	600
Db	541	GFKIINTASIOSLONNWKGCFSTFSVPDPLSAVTINASSRSGLDINDVPVYLKKR	600

```

QY          601 STEL 604
          |||
Db          601 STEL 604

          RESULT 14
          US-10-260-937-25
          ; Sequence 25, Application US/10260937
          ; Publication No. US20030220306A1
          ; GENERAL INFORMATION:
          ; APPLICANT: Simmons, Daniel
          ; APPLICANT: Chandrasekharan, N. Vishvanath
          ; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
          ; TITLE OF INVENTION: METHODS OF USE
          ; FILE REFERENCE: 07913-007001
          ; CURRENT APPLICATION NUMBER: US/10/260,937
          ; CURRENT FILING DATE: 2002-09-28
          ; PRIOR APPLICATION NUMBER: US 60/326,133
          ; PRIOR FILING DATE: 2001-09-28
          ; PRIOR APPLICATION NUMBER: US 60/373,225
          ; PRIOR FILING DATE: 2002-04-15
          ; PRIOR APPLICATION NUMBER: US 60/373,661
          ; PRIOR FILING DATE: 2002-04-16
          ; PRIOR APPLICATION NUMBER: US 60/411,575
          ; PRIOR FILING DATE: 2002-09-16
          ; NUMBER OF SEQ ID NOS: 89
          ; SOFTWARE: FastSeq for Windows Version 4.0
          ; SEQ ID NO 25
          ; LENGTH: 604
          ; TYPE: PRT
          ; ORGANISM: Bos taurus
          US-10-260-937-25

```

QY	1	MLAALLLCALVLAISHTANPCSSPCQNRGOWSVGFDQYKDCDTRIGFGENCSFEFL	60
Db	1	MLAARALLCAVALSAGANPCSSHPCONRGOWSVGFDQYKDCDTRIGFGENCSFEFL	60
QY	61	TRIKLFLKPTENTHYILLTEKGFWNVNNIPFLRNAIMSVLTSRSHLIDSPPTYNADY	120
Db	61	TRIKLFLKPTENTHYILLTHKGVNNIKNISFLRNIMRVLNRSRLIESPTYNVHY	120
QY	121	GYSKWEAFNSLSYYTRALPVVDDCPTPLGVKKKKLPDSNEIVEKLLIRKKEITPDQGS	180
Db	121	SYKSWEAFFNSLSYYTRALPVVDDCPTPMGVKKRKELPDSKEVKKVLLIRKKEITPDQGT	180
QY	181	NMRAFPFQHTHTEFKTDHKRGAFNLNGLGVDLNIYETLARQKLPFDGKKY	240
Db	181	NLMFAFPQHTHTEFKTDEPERGAFTKGNKHGVDLSHIVGESLEROHKLPFDGKKY	240
QY	241	QIIDGEMPRPVKQTOAMIVPPOVPEHLRPAVQGEVGLVPGMMVATIMLRHNRC	300
Db	241	QMINGEMPRPVKQTOVMIVPPIVPEHLKRAVQGEVGLVPGMLMATIMLRHNRC	300
QY	301	VLKQHEPMEDEOLFQTSRLILIGETIKIVIEDVYVHLSGYHFKLPDELLFNKQFOYQ	360
Db	301	VLKQHEPMEDEOLFQTSRLILIGETIKIVIEDVYVHLSGYHFKLPDELLFNQFOYQ	360
QY	361	NRIAAEFNTLYHMHPLPDTFQIHDQKNYQOQFIYNNSLIIEHGTQVVESEFTQIAGRV	420
Db	361	NRIAAEFNTLYHMHPLPDPVQIIOGQENYQOQFIYNNSVLIEHGTQVVESEFTQIARVR	420
QY	421	AGGRVPRPAVKVSAISDOSROMKYGSEFNRYRKMFKPESFEELTGEKEMSALEAL	480
Db	421	AGGRNLPAAVAKVSAISDOSREMYQSEFNRYRKLFLKPYESFEELTGEKEMAALEAL	480
QY	481	YGDIAVAVLYPALLVEKRPDAIFGETIWEAGAPFSLGLMGNTVICSPAYMKPSITFGEV	540
Db	481	YGDIDAMFYPALLVEKRPDAIFBEIWEAGAPFSLGLMGNTVICSPEYMKPSITFGEV	540

QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDLTKVTINASSSGLDINDPTVLKER 600
DB 541 GFKIINTASIOSLICSNNVKGCPFTSFVDPDLTKVTINASSSGLDINDPTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

DB 541 NTASIOSLICSNNVKGCPFTSFVDPDLTKVTINASSSGLDINDPTVLKERSTEL 599
Search completed: April 24, 2004, 07:27:00
JDB time : 75 secs

RESULT 15
US-09-949-293-31
; Sequence 31, Application US/09949293
; Publication No. US20030082550A1
; GENERAL INFORMATION:
; APPLICANT: Thomann, Hans-Ulrich
; APPLICANT: Wall, Kristian
; APPLICANT: Fitzgerald, Michael
; TITLE OF INVENTION: MUTATIONS OF THE CYCLOOXYGENASE-2 GENE
; FILE REFERENCE: TECH01-07
; CURRENT APPLICATION NUMBER: US/09/949,293
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/231,250
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-293-31

Query Match 89.7%; Score 2902; DB 10; Length 599;
Best local Similarity 88.8%; Pred. No. 1.4e-279;
Matches 532; Conservative 32; Mismatches 35; Indels 0; Gaps 0;

QY 6 LILCAVALSHSTANPCGSHPCONRGVMSVGFQYKCDCTRTGFGENCSTPEFLTRIKL 65
DB 1 MILCAVALSAGANPCGSHPCONRGVMSVGFQYKCDCTRTGFGENCSTPEFLTRIKL 60
QY 66 FLKPTNTVHYILTHFKGFMVNVNNIPFLRNALMSYVLTSSHLIDSPPTNADYGYKSW 125
DB 61 LLKPTNTVHYILTHFKGFMVNVNNIPFLRNALMSYVLTSSHLIDSPPTNADYGYKSW 120
QY 126 EAFNSLYTTRALPPVPDCCPTPLGVKGGKOLPDSNETIVEKLLRRKFIIPDQGSNMMA 185
DB 121 EAFNSLYTTRALPPVPDCCPTPLGVKGGKOLPDSNETIVEKLLRRKFIIPDQGSNMMA 180
QY 186 FFAQHTHOFKTHKRGPAFTNGLGHGVDLNHYGETLAROKRLFKDGKMYQITDG 245
DB 181 FFAQHTHOFKTHKRGPAFTNGLGHGVDLNHYGETLAROKRLFKDGKMYQITDG 240
QY 246 EMYPPTVKDTQAEIYPPQVEHLRFAGQEVFGLVPGIAMYATITLREHNRVCDVLKOE 305
DB 241 EMYPPTVKDTQAEIYPPQVEHLRFAGQEVFGLVPGIAMYATITLREHNRVCDVLKOE 300
QY 306 HPBWGDEQLFQTSRLILGETIKIYIEDYVOHLSGYHFKLPDPELLFNKQFOYQNR1AA 365
DB 301 HPBWGDEQLFQTSRLILGETIKIYIEDYVOHLSGYHFKLPDPELLFNKQFOYQNR1AA 360
QY 366 EFNLTLYMHPLLPPTFOIHDQKYNVQOFTYNNSTLLEGIQOFVESFTROIAAGVAGGRN 425
DB 361 EFNLTLYMHPLLPPTFOIHDQKYNVQOFTYNNSTLLEGIQOFVESFTROIAAGVAGGRN 420
QY 426 VPPAVQKVSQASIDQSRQMKYQSFNEYKRPMLKPYESFEELTGEKEMAELEALYGDID 485
DB 421 VPPAVQKVSQASIDQSRQMKYQSFNEYKRPMLKPYESFEELTGEKEMAELEALYGDID 480
QY 486 AVELYPALLVKRPDAIFGETIWEVGAAPSLSKGLMGANVICSPAYMKSTFGGEVGFQII 545
DB 481 AVELYPALLVKRPDAIFGETIWEVGAAPSLSKGLMGANVICSPAYMKSTFGGEVGFQII 540
QY 546 NTASIOSLICSNNVKGCPFTSFVDPDLTKVTINASSSGLDINDPTVLKERSTEL 604

Blank

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: April 24, 2004, 06:44:08 ; Search time 27 Seconds

(without alignments)
2151.840 Million cell updates/sec

Title: US-08-064-271-10

Perfect score: 3237

Sequence: 1 MARRALLCAVIALSHANP.....RSGLDINPTVLRKSTEL 604

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3230	99.8	604	2	A46150
2	2881.5	89.0	603	2	JC5063
3	2877	88.9	604	2	A49010
4	2868	88.6	604	2	JC2030
5	2726.5	84.2	603	2	A18630
6	2037	62.9	599	2	JH0259
7	2036.5	62.9	602	2	SE9198
8	2027.5	62.6	602	2	A35564
9	2026.5	62.6	602	2	A39782
10	2017.5	62.3	599	2	A29947
11	2004.5	61.9	600	2	S00561
12	1934.5	59.8	600	2	A28960
13	292	9.0	643	2	T03631
14	268.5	8.3	1475	2	T29809
15	250.5	7.3	1506	2	H96763
16	236	7.1	1506	2	T32909
17	231	7.1	977	2	T16232
18	228.5	7.1	739	2	T29407
19	223	6.9	655	2	T22448
20	219	6.8	1490	2	F88311
21	219	6.8	1490	2	T24502
22	212.5	6.6	718	2	T24502
23	204.5	6.3	773	2	D89010
24	204	6.3	818	1	JC4337
25	203	6.3	894	2	P00667
26	200	6.2	1313	2	T29027
27	196.5	6.1	1210	2	D88013
28	190	5.9	891	1	JN0867
29	181.5	5.6	1328	2	T23007

probable peroxidase
peroxidasein - frui
myeloperoxidase (E
peroxidase (EC 1.1
iodide peroxidase
related to feebly
iodide peroxidase
gene feebly protei
iodide peroxidase
iodide peroxidase
hypothetical prote
peroxinectin-like
peroxidase (EC 1.1
myeloperoxidase (E
myeloperoxidase (E
myeloperoxidase (E

30 173.5 5.4 724 2 T27858
31 172.5 5.3 1535 2 S46224
32 170 5.3 718 2 S06068
33 166.5 5.1 690 2 S28222
34 164.5 5.1 326 1 OPGIT
35 163.5 5.1 355 2 T49753
36 158.5 4.9 933 1 OPHUT
37 157 4.9 445 2 S70648
38 156 4.8 914 1 S07047
39 155 4.8 914 1 UN0550
40 150.5 4.6 1015 2 T32186
41 148.5 4.6 201 2 S53511
42 146.5 4.5 712 2 JC4935
43 146 4.5 745 1 OPHUM
44 146 4.5 825 2 C28894
45 146 4.5 830 2 B28894

ALIGNMENTS

RESULT 1
A46150
prostaglandin-endoperoxide synthase (EC 1.14.99.1) 2 precursor - human
N:Alternate names: cyclooxygenase-2; prostaglandin G/H synthase 2; prostaglandin H synth
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1993 #sequence revision 18-Nov-1994 #text change 04-Mar-2000
C:Accession: A46150; S54973; S46595; S66643; A46042; S50182
R:HLA, T.; Neilson, K.
Proc. Natl. Acad. Sci. U.S.A. 89, 7384-7388, 1992
A:Title: Human cyclooxygenase-2 cDNA.
A:Reference number: A46150; MUID:92366465; PMID:1380156
A:Accession: A46150
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-604 <HLA>
A:Cross-references: EMBL:U04636; NID:G181253; PIDN:AAA58433.1; PID:G181254
A:Experimental source: umbilical vein endothelial cells
A:Note: sequence extracted from NCBI backbone (NCBIN:110648, NCBIPI:110649)
R:Appleby, S.B., Ristimaki, A.; Neilson, K.; Narxo, K.; Hla, T.
Biochem. J. 302, 723-727, 1994
A:Title: Structure of the human cyclo-oxygenase-2 gene.
A:Reference number: S54973; MUID:95031910; PMID:7945196
A:Accession: S54973
A:Molecule type: DNA
A:Residues: 1-164, 'E', 166-604 <APP>
A:Cross-references: EMBL:U04636; NID:G496975; PIDN:AAA57317.1; PID:G496976
A:Experimental source: tissue placenta; cell-type endothelium
R:Kosaka, T.; Miyata, A.; Ihara, H.; Hara, S.; Sugimoto, T.; Takeda, O.; Takahashi, E.;
Eur. J. Biochem. 221, 889-897, 1994
A:Title: Characterization of the human gene (PTGS2) encoding prostaglandin-endoperoxide
A:Reference number: S46595; MUID:94237153; PMID:8181472
A:Accession: S46595
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-164, 'E', 166-604 <KOS>
A:Cross-references: EMBL:D28235; NID:G505116; PIDN:BA05698.1; PID:G1020089
A:Experimental source: Japanese peripheral blood
R:Memmole, L.P.; Liang, H.; Quintavalla, J.C.; Bowen, B.R.; Wasvary, J.; Miller, D.B.;
FEBS Lett. 371, 315-320, 1995
A:Title: Comparison of recombinant cyclooxygenase-2 to native isoforms: aspirin labelin
A:Reference number: S66643; MUID:96031160; PMID:7556619
A:Accession: S66643
A:Molecule type: protein
A:Residues: 18-21 <MEN>
R:Jones, D.A.; Carlton, D.P.; McIntyre, T.M.; Zimmerman, G.A.; Prescott, S.M.
J. Biol. Chem. 268, 9049-9054, 1993
A:Title: Molecular cloning of human prostaglandin endoperoxide synthase type II and dem
A:Reference number: A46042; MUID:932202069; PMID:8473346
A:Accession: A46042
A:Molecule type: mRNA
A:Residues: 1-164, 'E', 166-437, 'T', 439-604 <JON>
A:Cross-references: GB:U15326; NID:G291987; PIDN:AAA35803.1; PID:G291988

A:Experimental source: endothelial cells
 A:Note: sequence extracted from NCBI backbone (NCBIN:129879, NCBI:129881)
 R:Barnett, J.; Chow, J.; Ives, D.; Chou, M.; Mackenzie, R.; Osen, E.; Nguyen, B.; Tsing
 Biochim. Biophys. Acta 1209, 130-139, 1994
 A:Title: Purification, characterization and selective inhibition of human prostaglandin
 A:Reference number: S50181; MUID:95035046; PMID:7947975
 A:Accession: S50182
 A:Status: Preliminary
 A:Molecule type: protein
 A:Residues: 18-24 <BAR>
 C:Comment: The active site Ser-516 is predicted to be inhibited by aspirin acetylation.
 C:Genetics:
 A:Gene: GDB:PTGS2
 A:Cross-references: GDB:134805; OMTM:600262
 A:Map position: 1q25.2-1q25.3
 A:Introns: 18/1; 57/1; 105/1; 153/1; 213/3; 241/3; 324/1; 419/3; 469/1
 C:Function:
 A:Description: catalyzes the oxidative cyclization by oxygen of arachidonic acid to pro
 A:Pathway: prostaglandin biosynthesis
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology
 C:Keywords: chromoprotein; endoplasmic reticulum; glycoprotein; heme; iron; metalloprote
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-604/Product: prostaglandin-endoperoxide synthase 2 #status experimental <MAT>
 F:122-54/Domain: EGF homology <EGF>
 F:130-336/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:295/Binding site: heme iron (His) (axial ligand) #status predicted
 F:371,516/Active site: Tyr, Ser #status predicted

Query Match 99.8%; Score 3230; DB 2; Length 604;
 Best Local Similarity 99.8%; Pred. No. 2e-238;
 Matches 603; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLARALLICAVIALSHTNPPCCSHPCQNRGVMSVGFQYKDCDCTRTGFGNCSTPEFL 60
DB 1 MLARALLICAVIALSHTNPPCCSHPCQNRGVMSVGFQYKDCDCTRTGFGNCSTPEFL 60
QY 61 TRIKFLKPTPTVYIILTHFGKFNWVNNIPFLNAINSVYLSRSNIDSPPTYNADY 120
DB 61 TRIKFLKPTPTVYIILTHFGKFNWVNNIPFLNAINSVYLSRSNIDSPPTYNADY 120
QY 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOS 180
DB 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOS 180
QY 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOS 180
DB 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOS 180
QY 181 NMMPAFPAQHFTQHFPTDKHKGPAFTNGLGHVLDNHYGTTARQRLRLFQGGKMY 240
DB 181 NMMPAFPAQHFTQHFPTDKHKGPAFTNGLGHVLDNHYGTTARQRLRLFQGGKMY 240
QY 241 QIIDEMYPPTVKDQAEIYPPVPEHLRFVAVGVEFGLVGLMMVATIMLRHNRYCD 300
DB 241 QIIDEMYPPTVKDQAEIYPPVPEHLRFVAVGVEFGLVGLMMVATIMLRHNRYCD 300
QY 301 VLKQHPHPEWGBOLFTQSTSLILIGETIKIVIEDYVQHSNGYHFKLPDELLFNKQFOYQ 360
DB 301 VLKQHPHPEWGBOLFTQSTSLILIGETIKIVIEDYVQHSNGYHFKLPDELLFNKQFOYQ 360
QY 361 NRIAAEFNTLYMHMLPPTFQIHDQKYNVQOPIYNNSLILHGTQFVESFTQIAGRY 420
DB 361 NRIAAEFNTLYMHMLPPTFQIHDQKYNVQOPIYNNSLILHGTQFVESFTQIAGRY 420
QY 421 AGGRVNPVAVQKVSQASIDQSRQMKQSNFNRKRFMLKPYSEFELLTEKMSALEL 480
DB 421 AGGRVNPVAVQKVSQASIDQSRQMKQSNFNRKRFMLKPYSEFELLTEKMSALEL 480
QY 481 YGDIDAVELYPALLVEKPRDAIFGETWVEGAPFSLKLMGNVICSPPAYMKSTFGGEV 540
DB 481 YGDIDAVELYPALLVEKPRDAIFGETWVEGAPFSLKLMGNVICSPPAYMKSTFGGEV 540
QY 541 GQOINTASTOSLIGNVKGCPFTSFVDPDELIKVTITNASSSRGLDINPTVILKER 600
DB 541 GQOINTASTOSLIGNVKGCPFTSFVDPDELIKVTITNASSSRGLDINPTVILKER 600
QY 601 STEL 604

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Db 601 STEL 604

RESULT 2
 JC5063
 prostaglandin-endoperoxide synthase (EC 1.14.99.1) 2 precursor - sheep
 N:Alternate names: prostaglandin H synthase 2
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
 C:Accession: JC5063; S68339
 R:Zheng, V.; O'Sullivan, M.; Hussain, H.; Roswit, W.T.; Holtzman, M.J.
 Biochem. Biophys. Res. Commun. 227, 499-506, 1996
 A:Title: Molecular cloning, functional expression, and selective regulation of ovine pro
 A:Reference number: JC5063; MUID:97032794; PMID:8878543
 A:Contents: tracheal epithelial cells
 A:Accession: JC5063
 A:Molecule type: mRNA
 A:Residues: 1-603 <ZHA>
 A:Cross-references: GB:U68486; NID:q1703495; PIDN:ANCA8684.1; PID:q1703496
 R:Johnson, J.L.; Mims, J.; Buckel, S.D.; Dyer, R.D.; Maddipati, K.R.
 Arch. Biochem. Biophys. 324, 26-34, 1995
 A:Title: Purification and characterization of prostaglandin H synthase-2 from sheep plac
 A:Reference number: S68339; MUID:96095685; PMID:7503555
 A:Accession: S68339
 A:Molecule type: protein
 A:Residues: 17-52; 'G', 100, 'K', 102-115; 183-196; 247-252, 'H', 253-255, 'N', 257, 286-306; 444-455
 A:Experimental source: placental cotyledons
 A:Description: This enzyme mediates constitutive versus inducible prostanoid production.
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology
 C:Keywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:117-603/Product: prostaglandin-endoperoxide synthase #status predicted <MAT>
 F:21-53/Domain: EGF homology <EGF>
 F:276-290/Domain: transmembrane #status predicted <TM>
 F:52,129,395,579/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:370,515/Active site: Tyr, Ser #status predicted
 F:373/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 89.0%; Score 2881.5; DB 2; Length 603;
 Best Local Similarity 87.6%; Pred. No. 7.9e-212;
 Matches 529; Conservative 35; Mismatches 39; Indels 1; Gaps 1;

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QY 1 MLARALLICAVIALSHTNPPCCSHPCQNRGVMSVGFQYKDCDCTRTGFGNCSTPEFL 60
DB 1 MLARALLICAVVCG-ANPPCCSHPCQNRGVMSVGFQYKDCDCTRTGFGNCSTPEFL 59
QY 61 TRIKFLKPTPTVYIILTHFGKFNWVNNIPFLNAINSVYLSRSNIDSPPTYNADY 120
DB 60 TRIKFLKPTPTVYIILTHFGKFNWVNNIPFLNAINSVYLSRSNIDSPPTYNADY 119
QY 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOS 180
DB 120 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOS 179
QY 181 NMMPAFPAQHFTQHFPTDKHKGPAFTNGLGHVLDNHYGTTARQRLRLFQGGKMY 240
DB 180 NMMPAFPAQHFTQHFPTDKHKGPAFTNGLGHVLDNHYGTTARQRLRLFQGGKMY 239
QY 241 QIIDEMYPPTVKDQAEIYPPVPEHLRFVAVGVEFGLVGLMMVATIMLRHNRYCD 300
DB 240 QIIDEMYPPTVKDQAEIYPPVPEHLRFVAVGVEFGLVGLMMVATIMLRHNRYCD 299
QY 301 VLKQHPHPEWGBOLFTQSTSLILIGETIKIVIEDYVQHSNGYHFKLPDELLFNKQFOYQ 360
DB 300 VLKQHPHPEWGBOLFTQSTSLILIGETIKIVIEDYVQHSNGYHFKLPDELLFNKQFOYQ 359
QY 361 NRIAAEFNTLYMHMLPPTFQIHDQKYNVQOPIYNNSLILHGTQFVESFTQIAGRY 420
DB 360 NRIAAEFNTLYMHMLPPTFQIHDQKYNVQOPIYNNSLILHGTQFVESFTQIAGRY 419
QY 421 AGGRVNPVAVQKVSQASIDQSRQMKQSNFNRKRFMLKPYSEFELLTEKMSALEL 480
DB 421 AGGRVNPVAVQKVSQASIDQSRQMKQSNFNRKRFMLKPYSEFELLTEKMSALEL 480

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Db 420 AGRNLPAAVEKSKASLQSRKMKYQSNREKREPLKPYESFEELTGKEMAALEAL 479
 QY 481 YGDIDAVELLYPALIVEKRPDAIFGETWEVGAPEFLKMGVNICSPAYMKPSTFGGEV 540
 Db 480 YGIDAMELYPALIVEKRPDAIFGETWEAGAPFLKMGVNICSPAYMKPSTFGGEV 539
 QY 541 GQIINTASTIQLICNNVKGCPFTSGVDPDELTKVTINASSSRSGLDINPTVLKKE 600
 Db 540 GKRIINTASTIQLICNNVKGCPFTSGVDPDELTKVTINASSSRSGLDINPTVLKKE 599
 QY 601 STEL 604
 Db 600 STEL 603

RESULT 3
 A49010
 prostaglandin-endoperoxide synthase (EC 1.14.99.1), glucocorticoid-sensitive - mouse
 M:Alternate names: prostaglandin G/H synthase; prostaglandin synthase/cyclooxygenase
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Jan-1994 #sequence revision 18-Nov-1994 #text_change 17-Nov-2000
 C:Accession: A49010; A45379; A39854; A41583
 R:Flyback, R.P.; Rayneschek, C.; Macdonald-Bravo, H.; Dorfman, K.; Mattei, M.G.; Bravo, R.
 Cell Growth Differ. 3: 443-450, 1992
 A>Title: Identification of an immediate early gene, pghs-B, whose protein product has pr
 A:Reference number: A49010; MUID:93041378; PMID:1419907
 A:Accession: A49010
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-604 <RVS>
 A:Experimental source: NIH 3T3 cells
 A>Note: Sequence extracted from NCBI backbone (NCBI:117105)
 R:O'Banion, M.K.; Winn, V.D.; Young, D.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4888-4892, 1992
 A>Title: cDNA cloning and functional activity of a glucocorticoid-regulated inflammatory
 A:Reference number: A45379; MUID:92279232; PMID:1594589
 A:Accession: A45379
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-141, 'A', '143-584', 'H', '586-604' <OIB>
 A:Cross-references: GB:M8242; NID:G193637; PIDN:AAA37740.1; PID:G193638
 A>Note: Sequence extracted from NCBI backbone (NCBI:104202, NCBI:104203)
 R:Knjuba, D.A.; Fletcher, B.S.; Varnum, B.C.; Lim, R.W.; Herschman, H.R.
 J. Biol. Chem. 266, 12866-12872, 1991
 A>Title: TIS10, a phorbol ester tumor promoter-inducible mRNA from Swiss 3T3 cells, enc
 A:Reference number: A39854; MUID:91302297; PMID:1712772
 A:Accession: A39854
 A:Molecule type: mRNA
 A:Residues: 1-97, 'T', '99-141', 'A', '143-584', 'H', '586-604' <KJ>
 A:Cross-references: GB:M64291; NID:G200336; PIDN:AAA39924.1; PID:G200337
 R:O'Banion, M.K.; Sadowski, H.B.; Winn, V.; Young, D.A.
 J. Biol. Chem. 266, 23261-23267, 1991
 A>Title: A serum- and glucocorticoid-regulated 4-kilobase mRNA encodes a cyclooxygenase-
 A:Reference number: A41583; MUID:92078199; PMID:1744122
 A:Accession: A41583
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 281-300, 'L', '302-360' <OAB>
 C:Genetics:
 A:Gene: TIS10
 C:Superfamily: human prostaglandin-endoperoxide synthase, EGF homology
 C:Keywords: oxidoreductase
 F:21-54/Domain: EGF homology <EGF>

Query Match 88.9%; Score 2877; DB 2; Length 604;
 Best Local Similarity 86.9%; Pred. No. 1.7e-211;
 Matches 523; Conservative 39; Mismatches 40; Indels 0; Gaps 0;

QY 1 MLRAILLCAVLAISHTANPCGSHPCNRCGVMSVGFQYKCDTRTGFYGENCSTEFLL 60
 Db 1 MLFAVLLCAALGALISQAANPCSNPCQNRGCMSTGFQYKCDTRGFGFGENCTTEFL 60
 QY 61 TRIKLFLKPTPNVHYILTHFGKGVNWNIPFLRNALMSYVLTSRSHLIDSPPTNADY 120

Db 61 TRIKLFLKPTPNVHYILTHFGKGVNWNIPFLRNALMSYVLTSRSHLIDSPPTNADY 120
 QY 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVYKQKQLPDSNIEVKLLRRKFPDPOS 180
 Db 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVYKQKQLPDSNIEVKLLRRKFPDPOS 180
 QY 181 NMFAFAFHQFHQFHKDHRKGFATNGLGHGVDLNIYGETTLAROKRLFPQGRMKY 240
 Db 181 NMFAFAFHQFHQFHKDHRKGFATNGLGHGVDLNIYGETTLAROKRLFPQGRMKY 240
 QY 241 QIIDEMPTPTKDTQAEIMTYPOVBEHLRFVAVGOEVLVGLVMVATIMLRNRVCD 300
 Db 241 QVIGGEVVPPTKDTQAEIMTYPOVBEHLRFVAVGOEVLVGLVMVATIMLRNRVCD 300
 QY 301 VLKQHPBWDGOLFQTSRLILIGETIKIVIEDVYQHLSGYHFKLPDELLFNKQFOYQ 360
 Db 301 ILKQHPBWDGOLFQTSRLILIGETIKIVIEDVYQHLSGYHFKLPDELLFNKQFOYQ 360
 QY 361 NRFAEFNTLHMHPLPDTQIHDQKNYQOFTNNSTLLEHGTQFVSEFTROIAGRV 420
 Db 361 NRFAEFNTLHMHPLPDTQIHDQKNYQOFTNNSTLLEHGTQFVSEFTROIAGRV 420
 QY 421 AGRNVPPAVQKVSASIDQSRQMKYQSFNERYKRFMLKPYESFEELTGKEMAALEAL 480
 Db 421 AGRNVPPAVQKVSASIDQSRQMKYQSFNERYKRFMLKPYESFEELTGKEMAALEAL 480
 QY 481 YGDIDAVELLYPALIVEKRPDAIFGETWEVGAPEFLKMGVNICSPAYMKPSTFGGEV 540
 Db 481 YSDIDAVELLYPALIVEKRPDAIFGETWEVGAPEFLKMGVNICSPAYMKPSTFGGEV 540
 QY 541 GQIINTASTIQLICNNVKGCPFTSGVDPDELTKVTINASSSRSGLDINPTVLKKE 600
 Db 541 GFKIINTASTIQLICNNVKGCPFTSGVDPDELTKVTINASSSRSGLDINPTVLKKE 600
 QY 601 STEL 604
 Db 601 STEL 604

RESULT 4
 JC2030
 prostaglandin-endoperoxide synthase (EC 1.14.99.1) 2 precursor - rat
 M:Alternate names: cyclooxygenase-2
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text_change 04-Mar-2000
 C:Accession: JC2030; PC2015; S39783; A42167
 R:Kennedy, B.P.; Chan, C.C.; Culp, S.A.; Cromlish, W.A.
 Biochem. Biophys. Res. Commun. 197, 494-500, 1993
 A>Title: Cloning and expression of rat prostaglandin endoperoxide synthase (cyclooxygen
 A:Reference number: JC2030; MUID:94092121; PMID:7916614
 A:Accession: JC2030
 A:Molecule type: mRNA
 A:Residues: 1-604 <KEN>
 A:Cross-references: GB:L25925; NID:G414812; PIDN:AAA16477.1; PID:G414813
 A:Accession: PC2015
 A:Molecule type: protein
 A:Residues: 18-43 <KE2>
 R:Feng, L.; Sun, W.; Xia, Y.; Tang, W.W.; Chanmugam, P.; Soyoola, E.; Wilson, C.B.; Hwa
 Arch. Biochem. Biophys. 307, 361-368, 1993
 A>Title: Cloning two isoforms of rat cyclooxygenase: differential regulation of their e
 A:Reference number: S39783; MUID:94099619; PMID:8274023
 A:Accession: S39783
 A:Molecule type: mRNA
 A:Residues: 1-10, 'CPG', '14-57', 'R', '59-65', 'E', '67-95', 'IQS', '99-338', 'R', '340-343', 'Q', '345-349', '
 A:Cross-references: GB:S67722; NID:G460557; PIDN:AA829401.1; PID:G460558
 R:Strohs, J.; Richards, J.S.
 J. Biol. Chem. 267, 6382-6388, 1992
 A>Title: Purification and characterization of a novel, distinct isoform of prostaglandin

A:Reference number: A42167; MUID:92210620; PMID:1556140
 A:Accession: A42167
 A>Status: preliminary

A: Molecule type protein
 A: Residues: 18-43 <STR>
 C: Comment: This protein provides the prostanoids involved in inflammation and mitogenesis.
 C: Comment: The active site Ser-516 is predicted to be inhibited by aspirin acetylation.
 C: Superfamily: human prostaglandin-endoperoxide synthase; EGF homology
 C: Keywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase; tra
 F: 1-17/Domain: signal sequence #status predicted <Sig>
 F: 18-604/Product: prostaglandin-endoperoxide synthase #status predicted <Mat>
 F: 22-54/Domain: EGF homology <EGF>
 F: 227-291/Domain: transmembrane #status predicted <TM>
 F: 553,130,336,580/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F: 5371,516/Active site: Tyr, Ser #status predicted
 F: 374/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 88.6%; Score 2868; DB 2; Length 604;
 Best Local Similarity 86.4%; Pred. No. 8.5e-211;
 Matches 552; Conservative 40; Mismatches 42; Indels 0; Gaps 0;

QY	1	MLAALLICAVLAISHRANPCCHPCONRGVGVSDQYKCDCTRGFGENCSTPEFL	60
Db	1	MLFPAVALLICAAALASHANPCSCNRCGMSIGDQYKCDCTRGFGENCSTPEFL	60
QY	61	TRILKPLKPTNTGYHILLTFKGFNNVNNIPFLRNAMSIVLTSRSHLIDSPPTYADY	120
Db	61	TRILKLLKPTNTGYHILLTFKGYNNIVNNIPFLRNIMKIVLTSRSHLIDSPPTYVHY	120
QY	121	GYKSWEAESNLSYVTRALPVVDDCPPLGVYKKKQLPDSNEIVEKLLLRKKIPDPQGS	180
Db	121	GYKSWEAESNLSYVTRALPVVDDCPPLGVYKKKQLPDSKEVEKLLLRREFIPDQGT	180
QY	181	NMMAFAFPGHETHPGFTDKHKGAPFNGGSHGVDLNHIYGETLARORKLILFDGKKY	240
Db	181	NMMAFPAFQHTHPPFTDKRGPFTRKGLSHGVDLNHIYGETLDRQHKRLIFDQGLKY	240
QY	241	QIIDGEMPPPVKTKTOAEMIRPVQVPEHLRFVAGQEVFGILPGILMYATILREHNVCD	300
Db	241	QVIGSEVVPVVKDQVMDIYPRVPEHLRFVAGQEVFGILPGILMYATILREHNVCD	300
QY	301	VLKQHEPWPGBOLFOISRLLIGFTIKIYIEDVYQHSGHFLLKRPDELLFNKQRYQ	360
Db	301	ILKQHEPWPDBERLFQTSRLLIGFTIKIYIEDVYQHSGHFLLKRPDELLFNQOFOYQ	360
QY	361	NRIAEFTLILHMHPLBDTFQIDQKYNVQOQFIYNNISILHEHITQFVESFTQIAGR	420
Db	361	NRIASEFTLILHMHPLBDPTNIEQETFPQFLYNNISILHEGLAHVSEFTQIAGR	420
QY	421	AGRWNPVAVKVSQASIDQSRQMKYQSFENRYRRFMLKPYESEELTGEKMSAELEAL	480
Db	421	AGRWVPLVAVQAVAKASIDQSRMKYQSLNEFYRRFSLKPYTSEELTGEKMAAELEAL	480
QY	481	YGDIDAVELYPALLVEKRPDAIFGETMVEVGAPSLKGLMGNTICSPAVMKPPTGGEV	540
Db	481	YHDDIMAEVLPALLVEKRPDAIFGETMVEVGAPSLKGLMGNTICSPQYKAPPTGGEV	540
QY	541	GFQIINTASIOSILCNVKGCPFTSFVSVPDELLIKVTIINASSKSGLDIDNPVLLKER	600
Db	541	GFRINTASIOGLICNNVKGCFASFNQDDPQETKATATINASSASHSRADIDNPVLLIKR	600
QY	601	STEL 604	
Db	601	STEL 604	

RESULT 5
 A38630
 prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - chicken
 C: Species: Gallus gallus (chicken)
 C: Date: 14-Feb-1992 #sequence_rev15ion 14-Feb-1992 #text_change 21-Jul-2000
 C: Accession: A38630
 R: Xie, W.; Chipman, J. G.; Robertson, D. L.; Erikson, R. L.; Simmons, D. L.
 Proc. Natl. Acad. Sci. U.S.A. 88, 2692-2696, 1991
 A: Title: Expression of a mitogen-responsive gene encoding prostaglandin synthase is regu
 A: Reference number: A38630; MCID: 91187858; PMID: 1849272

A:Accession: A38630
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-603 <X1E>
 A:Cross-references: GB:M64990; NID:9212620; PTDN:AAA49050.1; PID:9212621
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology
 C:Keywords: oxidoreductase
 F:21-54/Domain: EGF homology <EGF>

Query Match 84.2%; Score 2726.5; DB 2; Length 603;
 Best Local Similarity 81.6%; Pred. No. 5.3e-200;
 Matches 493; Conservative 56; Mismatches 54; Indels 1; Gaps 1;

QY	1	MLADALLICAVLAISHTN	PCCSHPCQNRGVMSVGFQYKDCDCTRTGYGNCSTPEFL	60
DB	1	MLLPCALLAALLAGHAAN	PCCSLPCCNRGVMTGFFDECDCTRTGYGNCSTPEFL	60
QY	61	TRIKLFLKPTNTVHYIL	THFGKFMNVNNIPEFLNMAISVYLTSSHIDSPPTNADY	120
DB	61	TWLKILKPTNTVHYIL	THFGKGVNIIINISFLADTINRYLTSSHIDSPPTNSDY	120
QY	121	GYSKMEAFSNLSYYTRAL	PPVDDCPTPLGVYGGKQLPDSNIVEKILIRKRIIPDQGS	180
DB	121	SYKSMEASNLSYYTRSL	PPVGHDCPTPMGVGKKELPDSKILVEKFLIRKRIIPDQGT	180
QY	181	NMMRFAFFQHFHOFKTD	HKGRPAFTNGLGHGVDDNHIYGETLARQKILRLFKDGRKY	240
DB	181	NMMFFFAHFHOFKTD	HKKRPGFTKAYGGHGVDDNHIYGETLEQLKILRLKDGRLKY	240
QY	241	QIIDGEMVPTVKDQAE	KIYRPOVBEHLRFAVGOEFGLVPLGMVATITWLRHNRCVD	300
DB	241	QMIIDGEMVPTVKDQAE	KIYRPHVBEHLQFSVGQVFGVPLGMVATITWLRHNRCVD	300
QY	301	VLKQHPHPEWGDEQL	FQTSRLIIIGETIKIVIEDYQHLSGYHKKLPDEPLLNFQSRQYQ	360
DB	301	VLKQHPHPEWGDEQL	FQTSRLIIIGETIKIVIEDYQHLSGYHKKLPDEPLLNFQSRQYQ	360
QY	361	NRIAEFNTLYMHMLP	PTFQIHDQKYNVQOFIYNNLSILLEGITQFVESPTROLAGRY	420
DB	361	NRIAEFNTLYMHMLP	PTFQIHNEYTFQOFLYNNLSIMLEGHSHMWKVSFKQSGAGRY	420
QY	421	AGGRNVPPAVQVQAS	IDQSRQKYQSTNFRKRPMLKPYSEFELTGKENSABEFL	480
DB	421	AGGRNVPPAVQVQAS	IDQSRQKYQSTNFRKRPMLKPYSEFELTGKENSABEFL	480
QY	481	YGDIDAVELVPLAL	VEKRPDAIFGETWVEVGAFSLKGMGVICSPAYMKSTEGEV	540
DB	481	YGDIDAMELVPLAL	VEKRPDAIFGETWVEVGAFSLKGMGVICSPAYMKSTEGEV	540
QY	541	GFQIINTASIQSL	ICNNVKGCPFTSFSPDPELIKITVTINASSRSGLDINPTVILKER	600
DB	541	GFQIINTASIQSL	ICNNVKGCPFTSFSPDPELIKITVTINASSRSGLDINPTVILKER	600
QY	601	STEL	604	
DB	600	SAEL	603	

RESULT 6
 JH0259
 prostaglandin-endoperoxide synthase (EC 1.14.99.1) 1 precursor - human
 N:Alternate names: cyclooxygenase; prostaglandin G/H synthase; prostaglandin H synthase 1
 N:Contains: prostaglandin-endoperoxide synthase 1, splice form 2
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 04-Mar-2000
 R:Accession: JH0259; NM0225; A39937; B38146; A38146; S50181; A36746; S69169
 R:Rachabshi, Y.; Ueda, N.; Yoshimoto, T.; Yamamoto, S.; Yokoyama, C.; Miyata, A.; Tanabe, T.
 Biochem. Biophys. Res. Commun. 182, 433-438, 1992
 A:Title: Immunodiffinity purification and cDNA cloning of human platelet prostaglandin end
 A:Reference number: JH0259; M0ID:92134251; PMID:1734857
 A:Accession: JH0259
 A:Molecule type: mRNA
 A:Residues: 1-599 <TKAK>

A:Cross-references: GB:S78220; NID:g243971; PIDN:AA21215.1; PID:g243972
 A:Accession: PH0225
 A:Molecule type: protein
 A:Residues: 24-31 <TAK2>
 R:Funck, C.D.; Funck, L.B.; Kennedy, M.E.; Pong, A.S.; Fitzgerald, G.A.
 FASEB J. 5, 2304-2312, 1991
 A:Title: Human platelet/erythrocyte leukemia cell prostaglandin G/H synthase: cDNA cloning,
 A:Reference number: A39937; MUID:91317397; PMID:1907252
 A:Accession: A39937
 A:Molecule type: mRNA
 A:Residues: 1-599 <FUN>
 A:Cross-references: GB:M59979; NID:g189886; PIDN:AAA03630.1; PID:g189887
 R:Diaz, A.; Regnato, A.M.; Jimenez, S.A.
 J. Biol. Chem. 267, 10816-10822, 1992
 A:Title: Alternative splicing of human prostaglandin G/H synthase mRNA and evidence of
 nd tumor necrosis factor alpha.
 A:Reference number: A38146; MUID:92268138; PMID:1587858
 A:Accession: B38146
 A:Molecule type: mRNA
 A:Residues: 1-599 <DIA>
 A:Cross-references: GB:S36271; NID:g249625; PIDN:AA22217.1; PID:g249626
 A:Experimental source: lung fibroblast
 A:Note: sequence extracted from NCBI backbone (NCBIN:103945, NCBI:103946)
 A:Accession: A38146
 A:Molecule type: mRNA
 A:Residues: 1-395,433-599 <DIA>
 A:Cross-references: GB:S36219; NID:g249623; PIDN:AA22216.1; PID:g249624
 A:Experimental source: lung fibroblast
 A:Note: sequence extracted from NCBI backbone (NCBIN:103825, NCBI:103826)
 R:Barnett, J.; Chow, J.; Ives, D.; Chiu, M.; Mackenzie, R.; Osen, E.; Nguyen, B.; Tsing
 Biochem. Biophys. Acta 1209, 130-139, 1994
 A:Title: Purification, characterization and selective inhibition of human prostaglandin
 A:Reference number: S50181; MUID:95035046; PMID:7947975
 A:Accession: S50181
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 24-32 <BAR>
 R:Yokoyama, C.; Tanabe, T.
 Biochem. Biophys. Res. Commun. 165, 888-894, 1989
 A:Title: Cloning of human gene encoding prostaglandin endoperoxide synthase and primary
 A:Reference number: A36746; MUID:90086508; PMID:2512924
 A:Accession: A36746
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-11, 'L', 13-112, 'L', 114-377, 'T', 379-599 <YOK>
 A:Cross-references: GB:M31822; NID:g189898; PIDN:AAA6439.1; PID:g387018
 R:Ren, Y.; Loose-Mitchell, D.S.; Kulmacz, R.J.
 Arch. Biochem. Biophys. 316, 751-757, 1995
 A:Title: Prostaglandin H synthase-1: evaluation of C-terminus function.
 A:Reference number: S69169; MUID:95168661; PMID:7864630
 A:Accession: S69169
 A:Molecule type: protein
 A:Residues: 585-599 <REN>
 C:Genetics:
 A:Gene: GDB:PTGS1
 A:Cross-references: GDB:128070; OMIM:176805
 A:Map position: 9q32-9q33.3
 C:Function:
 A:Description: catalyzes the oxidative cyclization by oxygen of arachidonic acid to prod
 A:Pathway: prostaglandin biosynthesis
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology
 C:Keywords: alternative splicing; chromoprotein; endoplasmic reticulum; glycoprotein; he
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-599/Product: prostaglandin-endoperoxide synthase 1 #status experimental <MAT>
 F:24-35,433-599/Product: prostaglandin-endoperoxide synthase 1, splice form 2 #status E
 F:35-68/Domain: EGF homology <EGF>
 F:103,143,409/Binding site: carbonylate (Asn) (covalent) #status predicted
 F:308/Binding site: heme iron (His) (axial ligand) #status predicted
 F:384,529/Active site: Tyr, Ser #status predicted

Query Match 62.9%; Score 2037; DB 2; Length 599;
 Best Local Similarity 59.9%; Pred. No. 2,2e-147;
 Matches 370; Conservative 94; Mismatches 120; Indels 34; Gaps 4;

QY 2 LARALLGAVLAL-----SHTANPCGSHPCQNRVCVMISGFDQYKDCR 46
 Db 1 MRSLLRLRFLPLPLPVLADPGAPTPVNCQCYCQHQGICVRFGLDRYQCDCR 60
 QY 47 TGFYENCSTPEFLTRIKLTKPTPNTVYILTHKGFNNVNNIPELNAIMSYLTSR 106
 Db 61 TQSGPNCIRPLMTWIKRSLRSPSFTHFLHGRWMEFV-NATPEIMLRVLTVA 119
 QY 107 SHLIDSPPTYNADYGYKSMFAFNLSSYTRALPPVDDCPPLGVKSKQLPDSNIEVK 166
 Db 120 SMLISPPYNSAHDIYSWESFNSVSYTRILPSVKDPTMGTKGKKQLDAQLAAR 179
 QY 167 LILRRKFLPDPGCSMMFAFPAQHHTHOFKTDHKGAFNTGLGHVDLNIYGETLAR 226
 Db 180 FLNRKFLPDPGNTLMFAFPAQHHTHOFKTSKGKGFRTALGHVDLGIYGDNLER 239
 QY 227 QRLRLFPDQKMKYIILIDEMYPPTVKDQEMIPQVPEHLRFVAGQEVGLVGLMM 286
 Db 240 QYQLRFLFDGKLYQVLDGEMYPPEVEAPVLMHPRGIPPOSQAAVGOVFLGLML 299
 QY 287 YATWLRHNRVCDVLKOEHPWGDQIPQTSRLILIGETIKIVIEDVYQHLSGYFKLK 346
 Db 300 YATWLRHNRVCDVLKAEHPTWGDQIFQTRRLILIGETIKIVIEVYQHLSGYFKLK 359
 QY 347 FDPPELLFKQFOYONRIAEFNTLYHMHPLPDTQIHDQKYNQOFTYNNSTLLEKTT 406
 Db 360 FDPPELLFVQYQYRNRIMERNHLYHMHPLMPSDKVSOEYXQFENFMSLDYGYE 419
 QY 407 QVESFTROIAGRVAGNRPVAVQVQASIDQSRQKQSFNFYRKRFLKPYESPFE 466
 Db 420 ALVDAFSQIAGRIGCGNNMHILHVAVDVIREERKRLQFENYRKRFGMKPTTSQE 479
 QY 467 LTGEKMSAELEALYGDIDAVELYPALIVEKRPDPAIFGETWVEGAFPSKGLMGNYIC 526
 Db 480 LVGEKEMAAELEELIYGDIDALEFYGLILEKCHPMSIRGESMIEIGAFPSKGLGNPIC 539
 QY 527 SPAYWKEPTGGEVGFQIINIASIOSLICNNVKGCFPFSVPPELKITTYINASSRS 586
 Db 540 SPEWKEPTGGEVGFVKTATILKVLCLNFKTCYVSPVPAS----- 585
 QY 587 GLDDINPTVLKERSTEL 604
 Db 586 --QDDGPAV--ERPSTEL 599

RESULT 7
 prostaglandin G/H synthase 1 - rat
 S69198
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 10-Dec-1999
 A:Accession: S69198; S69199
 R:Kiltzler, J.W.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: S69198
 A:Accession: S69198
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-602 <KIT>
 A:Cross-references: EMBL:U18060; NID:g603051; PIDN:AAA85823.1; PID:g603052
 R:Kiltzler, J.; Hill, E.; Hardman, R.; Reddy, N.; Philpot, R.; Eling, T.E.
 Arch. Biochem. Biophys. 316, 856-863, 1995
 A:Title: Analysis and quantitation of splicing variants of the tPA-inducible PGHS-1
 A:Reference number: S69199; MUID:95168676; PMID:7864644
 A:Accession: S69199
 A:Molecule type: mRNA
 A:Residues: 61-602 <KIT>
 A:Cross-references: EMBL:U18060
 A:Note: only a part of the nucleic acid sequence is shown
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology
 C:Keywords: alternative splicing
 F:38-71/Domain: EGF homology <EGF>

Query Match	62.9%	Score 2036.5	DB 2	Length 602
Best Local Similarity	64.7%	Pred. No. 2.5e-147		
Matches 357	Conservative 90	Mismatches 104	Indels 1	Gaps 1
QY	19	NPCCSHPCQNRGVCMWVGFDQYKCDCTRTGTGYEENGSTEFELTRIKLFLKPTNTVHYIL	78	
Db	36	NPCCYPCQNGQVCVAFGLDHYQCDCRTGTGSPNCCTPEIWTMLRNSLRSPSFTHTLL	95	
QY	79	THEKGMWVNNVNIPEFLNAIMSYVLTSRSHLIDSPETPAADYGYKSWEASNSLSTYTRAL	138	
Db	96	THGYWIMEFY-NATFTREVLMRLVITVRSNLSPPTYNHAHDYIMESGNSVYTRILL	154	
QY	139	PPVPDCCPTLGYKGGKCOLPDSNEIVEKLLRKRFTIPDPGSGNMMEAFPAQHTHOEFKX	198	
Db	155	PSVPKXCPPTMGTKGKKQLPDHILNLRLLRREFTIPGCGTVLVAFPAQHTHOEFKX	214	
QY	199	DHRRGPAFTNLGHGYVDLNIYGETLARQKRLFKDQMKYQIIDGEMYPPIVYKOTQAE	258	
Db	215	SGKMGEGFTALGHGYVDLNIYGDSTLERQYHLRFKDGKLIKYOVLIDGEVYPPVSGQASVL	274	
QY	259	MIYPPQVPEHLRAVGGEGEVGLVPGIMVATYTLRHNRRVCVDLKOENPWEQEOIFQTS	318	
Db	275	MRRPPGVPPEKQAVAGEVGLPLGLMFSFTIMRBNRCVDLLKEHPRVWDEQIFQTT	334	
QY	319	RLILIGETITIVIEDVYOHLSGYHFKLPEPDELFNKQFOYQNRIAAEFTLYHMHPLP	378	
Db	335	RLILIGETIKIIIEVYQHLSGFYFLQDKPEPDELLFRQGFYRRIRIAEFNHLVHMHPLP	394	
QY	379	DTFQIHDQKYNVQOFTYNNSLLEHGITQVVESTROIAGRVAGRRVPRVAVQKVSQASI	438	
Db	395	DSFQVQGEYSYEBFLENTSMLVGYEALVDAFRRARIGGGRNFYDVHVAEDVI	454	
QY	439	DQSRQMYQSGFENFRKRFEMLKPYESFEELTGEKMSAFELALYGDIDAVELYPALVEKP	498	
Db	455	KBSREMRLOSPFNERKRFGLKPYTSPFQFCEKMALELBYGDIIDALFFQYMLKFC	514	
QY	499	RPDAIFGEIWEVGAFFSLKGLMGWNVICSPAYMKRSTFGESEVGFQIINTASIOSLICNV	558	
Db	515	QPNSLFGESEMIEMGAPFSLKGLGNPICSPBYMKRSTFEGDVGFINVINTASIKLVCINT	574	
QY	559	KGCFPTSFVVD 570		
Db	575	KTCGVYSFRVVD 586		
RESULT 8				
A:Accession: A35564				
prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - mouse				
C:Species: Mus musculus (house mouse)				
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 11-Jan-2000				
C:Accession: A35564				
R:Dimitt, D.L.; Bl-Haritch, E.A.; Kraemer, S.A.; Andrews, M.J.; Yao, E.F.; Armstrong, R.L.				
J. Biol. Chem. 265, 5192-5198, 1990				
A:Title: The aspirin and heme-binding sites of ovine and murine prostaglandin endoperoxid				
A:Reference number: A35564; MUID:90203007; PMID:2108169				
A:Accession: A35564				
A:Molecule type: mRNA				
A:Residues: 1-602 <DB>				
A:Cross-references: GB:M4141; NID:9200302; PIDN:AAA9913.1; PID:9200303				
C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology				
C:Keywords: oxidoreductase				
F:1-26/Domain: signal sequence #status predicted <SIG>				
F:27-602/Product: prostaglandin-endoperoxide synthase #status predicted <MAT>				
F:38-71/Domain: EGF homology <EGF>				
Query Match 62.6% Score 2027.5 DB 2 Length 602				
Best Local Similarity 65.0% Pred. No. 1.2e-146				
Matches 359 Conservative 86 Mismatches 106 Indels 1 Gaps 1				
QY	19	NPCCSHPCQNRGVCMWVGFDQYKCDCTRTGTGYEENGSTPEFLTRIKLFLKPTNTVHYIL	78	
Db	36	NPCCYPCQNGQVCVAFGLDHYQCDCRTGTGSPNCCTPEIWTMLRNSLRSPSFTHTLL	95	

QY THEGFNNVNNIIFELRNAINSVYLTSRSHLIDSPPTNADYGYKSWFAFSLMISYTRAL 138
 Db THGWIMLEFV-NATPIREVLMLVLTASNNLPSPEPTNSADYISMSFSFVSYYTRIL 154
 QY PPVDDCPTPLGVYKKQLPDSNEIVEKLLIRKRIIPDQSGNNMFAFAQHTHOFFKT 198
 Db PSVFKDCPTPTMGATGKKQLPVOILAQOLLRRERIIPAQGNILFAFAQHPTHQFFKT 214
 QY DHKSGPAFTNGLGHVDLNIHYGETLARQRKRLPRDGGMKYQIIDGEMYPPTVKTOAB 258
 Db SGRWGPFTKLGHGVDLGHLYGVDLBRQYHLRLRKDGKLYQVLDGEVYPSVEQASVL 274
 QY MTPPOVPEHLRFVAGQEVFGLVPLGMMYATIMLRKHNVCVLKQEHFEGWDEQLPQTS 318
 Db MRYPGPVPERQMAVGQEVFGLPLGLMFTSLMREHNVCOLLKEHPTWDEQLPQFT 334
 QY RLILIGETIKVIEEYVQHLGSHYHFKLKEPDELLRNKQYQYQNRILAEENTLYHMHPLRP 378
 Db RLILIGETIKVIEEYVQHLGSHYHFKLKEPDELLRFPAQYQYRNRILAMENNLHMHPLRP 394
 QY DTFOIHDKNVYVQCFIYNNNIIIEHGIQFVSEFTQIAGRVAAGNVPVAVQVQASAI 438
 Db NSFOVQSGEYSEYQGLFNTSMVLVDYGVLELVDAFNSQBRGRIGGGNPFYHVLHVAVDI 454
 QY DQSRQMYQSFNEVYKRRFMLKPYSEBELTGEKMSAELEALYGDIDAVEILPALLVERP 498
 Db KESREMRLOPFNEVYKRRFMLKPYSTFOELTGEKMAEAELELYGDIIDALEFYPGLLEKC 514
 QY RPDATFEGTMEVGAFPSTKGLMGAVTCSPAYMKPSTPGEGYFOFIINTASIOSLICNNV 558
 Db QPNSIFGSMILEMGAPFSLKGLNPLICSPERYWKISTFGDVGFNLVNTHSLKGLVCINT 574
 QY 559 KGCPTSFSPVD 570
 Db 575 KTCFVVSFRVPD 586
 RESULT 9
 S39782
 cyclooxygenase 1 - rat
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 20-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Dec-1999
 C.Accession: S39782
 R.Feng, L.; Sun, W.; Xia, Y.; Tang, W.W.; Chamugam, P.; Soyoola, E.; Wilson, C.B.; Hwang
 Arch. Biochem. Biophys. 307, 361-368, 1993
 A.Title: Cloning two isoforms of rat cyclooxygenase: differential regulation of their ex
 A.Reference number: S39782; MUID:94099619; PMID:8274023
 A.Accession: S39782
 A.Molecule type: mRNA
 A.Residues: 1-602 <PDB>
 A.Cross-References: GB:S67721; NID:9460555; PIDN:AA29400.1; PID:9460556
 C.Superfamily: human prostaglandin-endoperoxide synthase; EGF homology
 F:38-71/Domain: EGF homology <EGF>
 Query Match 62.6%; Score 2026.5; DB 2; Length 602;
 Best Local Similarity 64.2%; Pred. No. 1,4e-146;
 Matches 354; Conservative 92; Mismatches 104; Indels 1; Gaps 1;
 QY PCCSHPCQNRGVQSVGFDQYKDCCTRTGTYGNCSTPEFLTRIKLFLKPTPTVAKILT 79
 Db PCYYPCQNOGVQVPRGLDHYQDCDCTRTGYSGNCTIPELITWLRSLRSPSTHPLIT 96
 QY 80 HKKGFANVNNIIPFLRNALMSVYLTSRSHLIDSPPTNADYGYKSWFAFSLMISYTRALP 139
 Db HGWIWIEFV-NATPIREVLMLVLTASNNLPSPEPTNTAHDIISWESFSNVSYYTRILP 155
 QY 140 PVPDDCPTPLGVYKKQLPDSNEIVEKLLIRKRIIPDQSGNNMFAFAQHTHOFFKT 199
 Db 156 SVPKDCPTPTMGATGKKQLPDIHLAQRILLRERIIPAQGNILFAFAQHPTHQFFKT 215
 QY 200 HKRGAFTNGLGHVDLNIHYGETLARQRKRLPRDGGMKYQIIDGEMYPPTVKTOAB 259
 Db 216 TWKSGPFTKLGHGVDLGHLYGVDLBRQYHLRLRKDGKLYQVLDGEVYPSVEQASVYM 275

QY 439 DQSRQMKYQSNFNEKRPMLKPYESFEELTGKEMSALELALXGDIADVELYPALEIVKRP 498
 Db 453 KESHEVLRKQPFNEKRRKRPMPYTSFQELTSEKMPAALEELYGDIDALEFPGLLEK 512
 QY 499 RPDALFGEIWEVAGAFSLKGLMGVNLCSPAYMKRSTEGEGVQIINTASIOSLICNNV 558
 Db 513 HPSNIFGSMLEMAQFSLKGLMGVNLCSPEYKASTEGEGVNLVYATLTKLVCLNT 572
 QY 559 KGCPFTSVPDP 571
 Db 573 KTCFVVSFHVDP 585

RESULT 12

A28960
 prostaglandin-endoperoxide synthase (EC 1.14.99.1) G/H precursor - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 10-Dec-1999
 A:Accession: A28960
 R:DeWitt, D.L.; Smith, W.L.
 Proc. Natl. Acad. Sci. U.S.A. 85, 1412-1416, 1988
 A:Title: Primary structure of prostaglandin G/H synthase from sheep vesicular gland dete
 A:Reference number: A28960; MUID:88144447; PMID:3125548
 A:Accession: A28960
 A:Molecule type: mRNA
 A:Residues: 1-600 <DEM>
 A:Cross-references: GB:J03599; NID:g166035; PID:AAA31576.1; PID:g166036
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology
 C:Keywords: oxidoreductase
 F:36-69/Domain: EGF homology <EGF>

Query Match 59.8%; Score 1934.5; DB 2; Length 600;

Best Local Similarity 62.4%; Pred. No. 1.5e-139; Mismatches 120; Indels 1; Gaps 1;

Matches 345; Conservative 87; Mismatches 120; Indels 1; Gaps 1;

QY 19 NPCCSHPCQNRGVCMVSGFDQYKCDCTRTGFEYGCSTPEFLIRLKLKPTPTVHYIL 78
 Db 34 NPCCYVPOHQHOCIVRFLDRYQCDCTRIAPAPASRRYGPSSGRLCGPAPLSTFYL 93
 QY 79 THFKGFNVVNNIPFLRNALNSYVLTSHLIDSPPTYADYGYKSWKFLSYTRAL 138
 Db 94 THGRMLMDFV-NATFIRDTLMRLVLTVRSLNLPSPPTYADYLSWESFSVSYTRIL 152
 QY 139 PVPDPDCPTPLGVGKQKLPDSNEIVEKLLRRKFPDPQSGNMMAFAFAQHTQFEXT 198
 Db 153 PVPDPDCPTPLGVGKQKLPDAEFLSRRLRRKFPDPQSGNMMAFAFAQHTQFEXT 212
 QY 199 DHKGRPAFTNGLGHGVDLNLHIVGETLARQKRLRFKDGKMKYQIIDEMYPTVKDTQAE 258
 Db 213 SKMGEGFTRKALGHGVDLNLHIVGETLARQKRLRFKDGKMKYQIIDEMYPTVKDTQAE 272
 QY 259 MYPPPOVPHLRFANGQEVFGILPMATIMLRHNVCDVLKQEHMMDQLOFQTS 318
 Db 273 MYPPPOVPHLRFANGQEVFGILPMATIMLRHNVCDVLKQEHMMDQLOFQTS 332
 QY 319 RLILGETIKIYEDVVOHLSGHFKLKPDPPELLEKQFYQONRLAENLTYHMHPLP 378
 Db 333 RLILGETIKIYEDVVOHLSGHFKLKPDPPELLEKQFYQONRLAENLTYHMHPLP 392
 QY 379 DTFQIHDQKYNQOFLYNNLSLLEHGITQVESFTFQIAGRVAGRNVPVAVQVSQASI 438
 Db 399 DTFQIHDQKYNQOFLYNNLSLLEHGITQVESFTFQIAGRVAGRNVPVAVQVSQASI 452
 QY 439 DQSRQMKYQSNFNEKRPMLKPYESFEELTGKEMSALELALXGDIADVELYPALEIVKRP 498
 Db 453 KESHEVLRKQPFNEKRRKRPMPYTSFQELTSEKMPAALEELYGDIDALEFPGLLEK 512
 QY 499 RPDALFGEIWEVAGAFSLKGLMGVNLCSPAYMKRSTEGEGVQIINTASIOSLICNNV 558
 Db 513 HPSNIFGSMLEMAQFSLKGLMGVNLCSPEYKASTEGEGVNLVYATLTKLVCLNT 572
 QY 559 KGCPFTSVPDP 571
 Db 573 KTCFVVSFHVDP 585

Db 573 KTCFVVSFHVDP 585

RESULT 13

103631
 oxygenase, pathogen-induced - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
 A:Accession: T03631
 R:Sanz, A.; Moreno, J.I.; Castresana, C.
 submitted to the EMBL Data Library, July 1998
 A:Description: PLOX, a new pathogen-induced oxygenase with homology to animal cyclooxygen
 A:Reference number: 214980
 A:Accession: T03631
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-643 <SAN>
 A:Cross-references: EMBL:AJ007630; NID:e1318722; PID:e1318723
 A:Experimental source: cultivar petiole Havana SRI
 C:Genetics:
 A:Gene: plox

Query Match 9.0%; Score 292; DB 2; Length 643;

Best Local Similarity 21.4%; Pred. No. 3.8e-14; Mismatches 192; Indels 196; Gaps 19;

Matches 127; Conservative 78; Mismatches 192; Indels 196; Gaps 19;

QY 65 LFLKPTPTVH-----YILTHFKGFNVVNNIPFLRNALNSYVLTSHLIDSPPTYADYGYKSWKFLSYTRAL 107
 Db 11 LILSPLRPFHKKDLHDIERMTLSKLLFLVHLVDKLNLMHRLPVLIGLL---YLGAR 67
 QY 108 HLIDSPPTYN-----ADYGYKSWKFLSYTRAL 142
 Db 68 HLHGE---YNLINVGKPTIGVRSNPDHRYTADKYNDDPENAGSELSEFGRMNLVVD 124
 QY 143 DDCEPPLGVGKQKLPDSNEIVEKLLRRKFPDPQSGNMMAFAFAQHTQFEXT 193
 Db 125 Q-----HNLKKPDMVAVATKLLARNFVDTSKQFMTAASVIQFMHIDHLEDT 176
 QY 194 -----OFFKTHKGRPAFTNGLGH-----GVDLNLHIVGETLARQ 227
 Db 177 KOELKAABEVAASQCEPLSFRPFKTELPTGVELEKTHLNTPTPMWGSALYGSNAEVL 236
 QY 228 RLRLFLKDGKMKYQI---ID--GEYTPYVKDTQAEKITPPQVPEHFRVAGQEVRL 280
 Db 237 KVRFTFGKGLKLSADGLLEIDKNGKIIISGVRRNWA----- 273
 QY 281 VGLMMYATIMLRHNVCDVLKQEHMMDQLOFQTSRLILGETIKIYEDVVOHLSGH 340
 Db 274 --GLSALQALFVQEHNSVCDALKKEYPLEBEDLYRHARLVTSAYIAKVHTIDWYEL-- 329
 QY 341 YHFKLPDPPEL-----LFNKQFO-----YONRLAEEF 367
 Db 330 ---LKTDTLAGMANVYGLLKKFKDPFGHVGSLIGFVGMKKPENYGVYSLTEEF 385
 QY 368 NTLVHMHPLPDTFOIDQKYNQOFLYNNLSLLEHGITQVESFTFQIAGRVAGRNVPVAVQVSQASI 411
 Db 386 TSVYRMHQLLPKQLRINDATPGPKSLPLTNEPLLELIGSGKGLSKLIGFTKQWVS 445
 QY 412 FTRQIAGV-----AGRNVPVAVQVSQASIDQSRQMKYQSNFNEKRPMLKPYESFEELTGKEMSALELALXGDIADVELYPALEIVKRP 455
 Db 446 MGHQCGALELNNVYMMRDLPDQVDTGDRPDHID-LALETYDRRESVARYNEFRG 504
 QY 456 FMLKPYESFEELTGKEMSALELALYDIDAVEIVPALLVEKRP 507
 Db 505 MGIPIISKWEDLTDDBEVINTLGEVYGDVVEELDMVGAARKKIKGFAISRT 557

RESULT 14

T29809
 hypothetical protein C46A5.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 A:Accession: T29809

[illegible]

B/ANK

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 24, 2004, 04:53:43 / Search time 18 Seconds
(without alignments)
1747.243 Million cell updates/sec

Title: US-08-064-271-10
Perfect score: 3237
Sequence: 1 MRAALLCAVALSHSTNP.....RSLDDINPTVLKERSTEL 604

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3237	100.0	604	1	PGH2_HUMAN
2	2971	91.8	604	1	PGH2_RABIT
3	2938	90.8	604	1	PGH2_HORSE
4	2923	90.3	604	1	PGH2_BOVIN
5	2892	89.3	604	1	PGH2_CAVPO
6	2881.5	89.0	603	1	PGH2_SHEEP
7	2873	88.8	604	1	PGH2_MOUSE
8	2868	88.6	604	1	PGH2_RAT
9	2828	87.4	604	1	PGH2_MOUSE
10	2726.5	84.2	603	1	PGH2_CHICK
11	2037	62.9	599	1	PGH1_HUMAN
12	2036.5	62.9	602	1	PGH1_RAT
13	2027.5	62.6	602	1	PGH1_MOUSE
14	2016.5	62.3	600	1	PGH1_SHEEP
15	1004	31.0	259	1	PGH1_BOVIN
16	300.5	9.3	978	1	LIDS_GAERG
17	170	5.3	718	1	PERM_MOUSE
18	166.5	5.1	690	1	PERO_DROME
19	164.5	5.1	926	1	PERP_PIG
20	158.5	4.9	933	1	PERP_HUMAN
21	156	4.8	914	1	PERP_RAT
22	155	4.8	914	1	PERP_MOUSE
23	149	4.6	933	1	PERP_CANFA
24	146.5	4.5	712	1	PERL_HUMAN
25	146	4.5	745	1	PERM_HUMAN
26	125.5	3.9	1363	1	NX1A_CHICK
27	122.5	3.8	882	1	CJBA_BACUH
28	122.5	3.8	1471	1	NX1A_HUMAN
29	122.5	3.8	1514	1	NX1A_RAT
30	122.5	3.8	1530	1	NX1A_BOVIN
31	121.5	3.8	712	1	PERL_BOVIN
32	118.5	3.7	1287	1	RPO1_POWPV
33	118	3.6	715	1	PERE_HUMAN

34	115	3.6	3135	1	S230_PLAFO
35	113	3.5	886	1	SDP1_HAEIN
36	110.5	3.4	1529	1	SLR2_HUMAN
37	109	3.4	2471	1	NTC2_HUMAN
38	108.5	3.4	674	1	ETP1_MSEPV
39	108.5	3.4	2165	1	RRLP_HRSVA
40	108	3.3	716	1	PERE_MOUSE
41	107.5	3.3	1541	1	NX3A_HUMAN
42	107.5	3.3	1578	1	NX3A_RAT
43	107	3.3	718	1	LSR2_DROME
44	107	3.3	1072	1	HSR2_RAT
45	105	3.2	570	1	FBP3_STRPU

ALIGNMENTS

RESULT 1
ID PGH2_HUMAN STANDARD; PRT; 604 AA.
AC P35354; O16875;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Prostaglandin G/H synthase 2 precursor (BC 1.14.99.1) (Cyclooxygenase -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).
DE PTGS2 OR COX2.
GN PTGS2 OR COX2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=9332069; PubMed=8473346;
RA Jones D.A., Carlton D.P., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
RT "Molecular cloning of human prostaglandin endoperoxide synthase type II and demonstration of expression in response to cytokines";
RT J. Biol. Chem. 268:9049-9054(1993).
RN [12]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=92366465; PubMed=1380156;
RA Hla T., Neilson K.;
RT "Human cyclooxygenase-2 cDNA";
RT Proc. Natl. Acad. Sci. U.S.A. 89:7384-7388(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Periphera blood;
RX MEDLINE=94237153; PubMed=8181472;
RA Kosaka T., Miyata A., Ihara H., Hara S., Sugimoto T., Takeda O., Takahashi E.I., Yanabe T.;
RT "Characterization of the human gene (PTGS2) encoding prostaglandin-endoperoxide synthase 2";
RT Eur. J. Biochem. 221:889-897(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95031910; PubMed=7945196;
RA Appleby S.B., Ristimaki A., Neilson K., Narko K., Hla T.;
RT "Structure of the human cyclo-oxygenase-2 gene";
RT Biochem. J. 302:723-727(1994).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS HIS-228; ALA-428; ALA-511 AND ARG-587.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schekwitz W.S., Sherwood J.K., Wiltrak L.A., Nickerson D.A.;
RT Submitted (FEB-2003) to the EMBL/GenBank/DBO databases.
RN [6]
RP SEQUENCE FROM N.A.

RA Coville G.;
 RT Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Datchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: May have a role as a major mediator of inflammation
 CC and/or a role for prostanoil signaling in activity-dependent
 CC plasticity.
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
 CC H2 + A + H(2)O.
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
 CC molecule (By similarity).
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
 CC arachidonate; first step.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
 CC -1- INDUCTION: By cytokines and mitogens.
 CC -1- DISEASE: Likely to play a role in inflammatory diseases such as
 CC rheumatoid arthritis.
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
 CC peroxidase.
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
 CC inflammatory drugs such as aspirin.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
 CC -----
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 CC -----
 DR EMBL: L15326; AAA35803.1; -;
 DR EMBL: M90100; AAA58433.1; -;
 DR EMBL: D28235; BAA05698.1; -;
 DR EMBL: U04636; AAA57317.1; -;
 DR EMBL: AY229989; AAC38056.1; -;
 DR EMBL: AL033533; CAB41240.1; -;
 DR EMBL: BC013734; AAH13734.1; -;
 DR PIR: A46150; A46150.
 DR HSSP: Q05769; 1CVU.
 DR GeneW: HGNC:9605; PTGS2.
 DR MIM: 600262; -;
 DR GO: GO:0005737; C:cytoplasm; TAS.
 DR GO: GO:0004666; F:prostaglandin-endoperoxide synthase activity; TAS.
 DR GO: GO:0006928; P:cell motility; TAS.
 DR GO: GO:0007582; P:physiological processes; TAS.
 DR GO: GO:0006933; P:prostaglandin metabolism; TAS.
 DR InterPro: IPR002007; Anm_peroxidase.
 DR InterPro: IPR006209; EGF_like.

DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF03098; An_peroxidase; 1.
 DR Pfam: PF00008; EGF; 1.
 DR PRINTS: PR00457; AMPEOXIDASE.
 DR SMART: SM00181; EGF; 1.
 DR PROSITE: PS00022; EGF_1; FALSE NEG.
 DR PROSITE: PS01186; EGF_2; FALSE NEG.
 DR PROSITE: PS0026; EGF_3; 1.
 DR PROSITE: PS50292; PEROXIDASE; 1.
 DR OXIDOREDUCTASE: Dioxygenase; Peroxidase; Glycoprotein;
 KM Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane;
 KM Polymorphism.
 FT FT SIGNAL 1 17
 FT CHAIN 18 604
 FT DOMAIN 18 55
 FT DISULFID 21 32
 FT DISULFID 26 42
 FT DISULFID 44 54
 FT DISULFID 22 145
 FT DISULFID 555 561
 FT ACT SITE 193 193
 FT ACT SITE 371 371
 FT METAL 374 374
 FT SITE 516 516
 FT CARBOHYD 53 53
 FT CARBOHYD 130 130
 FT CARBOHYD 396 396
 FT CARBOHYD 580 580
 FT VARIANT 1 1
 FT VARIANT 228 228
 FT VARIANT 428 428
 FT VARIANT 488 488
 FT VARIANT 511 511
 FT VARIANT 587 587
 FT CONFLICT 165 165
 FT CONFLICT 438 438
 SQ SEQUENCE 604 AA; 68996 MM; 72PBD699F6128519 CRC64;
 Query Match 100.0%; Score 3237; DB 1; Length 604;
 Best local similarity 100.0%; Pred. No. 3; 9e-245;
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 M A R A L L L C A V A L S T A N P C S H P C O N R G V C S V G F D Y K C C C T T G F G N C S T P E F L 60
 DB 1 M A R A L L L C A V A L S T A N P C S H P C O N R G V C S V G F D Y K C C C T T G F G N C S T P E F L 60
 QY 61 T R I K L F L K P T P N T V A H I L T H F K G F M V V N N I P L T R A N A I M S Y V L T S R S H L I D S P P T Y N A D Y 120
 DB 61 T R I K L F L K P T P N T V A H I L T H F K G F M V V N N I P L T R A N A I M S Y V L T S R S H L I D S P P T Y N A D Y 120
 QY 121 G Y K S W E A F S N L S Y T T A L P P V P D C P T P L G V K G K K Q L P D S N E I V E K L L R R K T I P D P Q S 180
 DB 121 G Y K S W E A F S N L S Y T T A L P P V P D C P T P L G V K G K K Q L P D S N E I V E K L L R R K T I P D P Q S 180
 QY 121 G Y K S W E A F S N L S Y T T A L P P V P D C P T P L G V K G K K Q L P D S N E I V E K L L R R K T I P D P Q S 180
 DB 121 G Y K S W E A F S N L S Y T T A L P P V P D C P T P L G V K G K K Q L P D S N E I V E K L L R R K T I P D P Q S 180
 QY 181 N M M E A F P A C H F T H P F K T H K R G P A C T N G L G H G V D L N H I Y G E T L A R Q R K L R L P K D G K M Y 240
 DB 181 N M M E A F P A C H F T H P F K T H K R G P A C T N G L G H G V D L N H I Y G E T L A R Q R K L R L P K D G K M Y 240
 QY 241 Q I I D G M Y P P T V K D T Q A E M I T P P V E H L R F A V G E V F G L V P G L M Y A T I M L R E H N R V C D 300
 DB 241 Q I I D G M Y P P T V K D T Q A E M I T P P V E H L R F A V G E V F G L V P G L M Y A T I M L R E H N R V C D 300
 QY 301 V L K O E H P E W G D E O L F O T S R L I L I G E T I K I V I D Y V O H L S Y H R K L K P D E L L F N K O P O Y O 360
 DB 301 V L K O E H P E W G D E O L F O T S R L I L I G E T I K I V I D Y V O H L S Y H R K L K P D E L L F N K O P O Y O 360

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QY 361 NRIAEFNTLYMHPLPDTFQIHDKYNYQGFYNNSSILLEGITQFVESFTROJAGRY 420
DB 361 NRIAEFNTLYMHPLPDTFQIHDKYNYQGFYNNSSILLEGITQFVESFTROJAGRY 420
QY 421 AGGRNVPPAVQKVSQASIDSRQMKYQSFNEVYKRFMLKPYSEFELTGKEMSALEAL 480
DB 421 AGGRNVPPAVQKVSQASIDSRQMKYQSFNEVYKRFMLKPYSEFELTGKEMSALEAL 480
QY 481 YGDDIDAVELYPALLVKEKRPDAIFGETMVEVGAPFSLKGLMGVICSPPAWKSTFGGEV 540
DB 481 YGDDIDAVELYPALLVKEKRPDAIFGETMVEVGAPFSLKGLMGVICSPPAWKSTFGGEV 540
QY 541 GFOIINTVASTQSIQNNVKGCPFTSFSVPDEPILIKTVTINASSRSGLDINPTVLLKER 600
DB 541 GFOIINTVASTQSIQNNVKGCPFTSFSVPDEPILIKTVTINASSRSGLDINPTVLLKER 600
QY 601 STEL 604
DB 601 STEL 604

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RESULT 2

PGH2_RABIT STANDARD; PRT; 604 AA.

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AC 002768;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase
  2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2
  synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).
GN PTGS2 OR COX2 OR COX-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=97939071; PubMed=9249588;
RA Guan Y., Chang M., Cho W., Zhang Y., Redha R., Davis L., Chang S.,
  Dubois R.N., Hao C.M., Breyer M.;
RT "Cloning, expression, and regulation of rabbit cyclooxygenase-2 in
  renal medullary interstitial cells.";
RL Am. J. Physiol. 273:F18-F26(1997).
CC -1- FUNCTION: May have a role as a major mediator of inflammation
  and/or a role for prostanoid signaling in activity-dependent
  plasticity.
CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
  H2 + A + H(2)O.
CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
  molecule (By similarity).
CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
  arachidonate, first step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
CC -1- TISSUE SPECIFICITY: Highest expression in kidney and urinary
  bladder.
CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
  peroxidase.
CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
  inflammatory drugs such as aspirin.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
CC -----
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CC EMBL: U97696; AAB71222.1; -.
DR HSP; 005769; 1CVY.
DR InterPro: IPR002007; Anm_peroxidase.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF03098; An_peroxidase; 1.
DR PRINTS: PR00457; ANPEROXIDASE.
DR SMART: SM00181; EGF; 1.
DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; FALSE_NEG.
DR PROSITE: PS50026; EGF_3; 1.
DR PROSITE: PS50292; PEROXIDASE_3; 1.
DR OXidoreductase; Dioxygenase; Peroxidase; Glycoprotein;
  Heme; Iron; Signal; Membrane.
KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.
FT SIGNAL 1 17
FT CHAIN 18 604
FT DOMAIN 18 55
FT ACT_SITE 193 193
FT ACT_SITE 371 371
FT METAL 374 374
FT SITE 516 516
FT DISULFID 21 32
FT DISULFID 26 42
FT DISULFID 44 54
FT DISULFID 22 145
FT DISULFID 555 561
FT CARBOHYD 53 53
FT CARBOHYD 130 130
FT CARBOHYD 396 396
FT CARBOHYD 580 580
SQ SEQUENCE 604 AA; 69007 MW; C52P9FBC1F493D7 CR664;

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Query Match 91.8%; Score 2971; DB 1; Length 604;
 Best Local Similarity 89.9%; Pred. No. 2,4e-224;
 Matches 543; Conservative 35; Mismatches 26; Indels 0; Gaps 0;

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QY 1 MLARALLCAVALALSHHTANPCQSHPCQNGVCMGSGFDYKDCDCTRTGFGNCSPEEL 60
DB 1 MLARALLCAVALALSHHTANPCQSHPCQNGVCMGSGFDYKDCDCTRTGFGNCSPEEL 60
QY 61 TRIKLFLKPTNTVHYIILTFKGFNVNNTIPELNAIMSYVLTSRSHLIDSPPTNADY 120
DB 61 TRIKLFLKPTNTVHYIILTFKGFNVNNTIPELNAIMSYVLTSRSHLIDSPPTNADY 120
QY 121 GYKSEADSNLSYTRALPPVDDCPTPLGVKKQKQLPDSNEIVEKLLIRKFTPDGGS 180
DB 121 GYKSEADSNLSYTRALPPVDDCPTPLGVKKQKQLPDSNEIVEKLLIRKFTPDGGS 180
QY 121 NYKSWAESNLSYTRALPPVDDCPTPLGVKKQKQLPDSNEIVEKLLIRKFTPDGGS 180
DB 121 NYKSWAESNLSYTRALPPVDDCPTPLGVKKQKQLPDSNEIVEKLLIRKFTPDGGS 180
QY 181 NMMFAFPFQHFTHQFKTDHKGPAFTNGLGHVLDNHYETLARQRKLRFKQGMKY 240
DB 181 NMMFAFPFQHFTHQFKTDHKGPAFTNGLGHVLDNHYETLARQRKLRFKQGMKY 240
QY 241 QIIDEMYPPTVKDQOAEIMYPPQVPEHLRFVAGQEVGLVGLMMYATITLREHNRVCD 300
DB 241 QIIDEMYPPTVKDQOAEIMYPPQVPEHLRFVAGQEVGLVGLMMYATITLREHNRVCD 300
QY 241 QYIDEEVYPTVKDQOAEIMYPPQVPEHLRFVAGQEVGLVGLMMYATITLREHNRVCD 300
DB 241 QYIDEEVYPTVKDQOAEIMYPPQVPEHLRFVAGQEVGLVGLMMYATITLREHNRVCD 300
QY 301 VLKQHPFWGDBQLFQTSRLIIGRTIKIVIEDYQHLSGYHFKLPDELLFNQOFQY 360
DB 301 VLKQHPFWGDBQLFQTSRLIIGRTIKIVIEDYQHLSGYHFKLPDELLFNQOFQY 360
QY 361 NRIAEFNTLYMHPLPDTFQIHDKYNYQGFYNNSSILLEGITQFVESFTROJAGRY 420
DB 361 NRIAEFNTLYMHPLPDTFQIHDKYNYQGFYNNSSILLEGITQFVESFTROJAGRY 420
QY 421 AGGRNVPPAVQKVSQASIDSRQMKYQSFNEVYKRFMLKPYSEFELTGKEMSALEAL 480
DB 421 AGGRNVPPAVQKVSQASIDSRQMKYQSFNEVYKRFMLKPYSEFELTGKEMSALEAL 480
QY 481 YGDDIDAVELYPALLVKEKRPDAIFGETMVEVGAPFSLKGLMGVICSPPAWKSTFGGEV 540
DB 481 YGDDIDAVELYPALLVKEKRPDAIFGETMVEVGAPFSLKGLMGVICSPPAWKSTFGGEV 540

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QY 541 GFOIINTASTIQSILCNVKGCPPTSGVPPPELTKVTYNASSSGGLDINPTVLKER 600
 Db 541 GFKIVNTASTIOSILCNVKGCPPTSGVPPPELTKVTYNASSSGGLDINPTVLKER 600
 QY 601 STEL 604
 Db 601 STEL 604

RESULT 3
 PGH2_HORSE STANDARD; PRT; 604 AA.

AC 019183;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).
 GN PTGS2 OR COX2.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OC NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98187796; PubMed=9528947;
 RA Boerboom D.; Sirotis U.;
 RT "Molecular characterization of equine prostaglandin G/H synthase-2 and regulation of its messenger ribonucleic acid in preovulatory follicles".
 RT Endocrinology 139:1662-1670(1998).
 CC -1- FUNCTION: May have a role as a major mediator of inflammation and/or a role for prostanoil signaling in activity-dependent plasticity.
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin H2 + A + H(2)O.
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per molecule (By similarity).
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from arachidonate; first step.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a peroxidase.
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-inflammatory drugs such as aspirin.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
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 CC
 DR EMBL; AF027335; AAC48808.1; -;
 DR EMBL; AF027334; AAC07911.1; -;
 DR HSSP; 005769; 3PGH.
 DR InterPro; IPR002007; Anim_peroxidase.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PF03098; An_peroxidase; 1.
 DR Pfam; PF03008; EGF; 1.
 DR PRINTS; PRO0457; ANPEROXIDASE.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS50026; EGF_3; 1.

DR PROSITE; PS50292; PEROXIDASE_3; 1.
 KW Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;
 KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.
 FT SIGNAL 1 17
 FT CHAIN 18 604
 FT DOMAIN 18 55
 FT ACT_SITE 193 193
 FT ACT_SITE 371 371
 FT METAL 374 374
 FT SITE 516 516
 FT DISULFID 21 32
 FT DISULFID 26 42
 FT DISULFID 44 54
 FT DISULFID 22 145
 FT DISULFID 555 561
 FT CARBOHYD 53 53
 FT CARBOHYD 130 130
 FT CARBOHYD 396 396
 FT CARBOHYD 580 580
 SQ SEQUENCE 604 AA; 68847 MW; 28792F7EB513068 CRC64;

Query Match 90.8%; Score 2938; DB 1; Length 604;
 Best Local Similarity 88.9%; Pred. No. 9e-222;
 Matches 537; Conservative 35; Mismatches 32; Indels 0; Gaps 0;

QY 1 MAAAILLCAVLAALSTANAPCCSHPCQNGVCMVSGFDQKDCCTRTGYGNCSTPEFL 60
 Db 1 MAARALLCAVLAALSTANAPCCSHPCQNGVCMVSGFDQKDCCTRTGYGNCSTPEFL 60
 QY 61 TRIKFLKPTPTVHILTHFKGFMVNNIPRLNAINSVYLTSSHLIDSPPTNADY 120
 Db 61 TRIKFLKPTPTVHILTHFKGFMVNNIPRLNAINSVYLTSSHLIDSPPTNADY 120
 QY 121 GYKSWFAFNSLSTYTBALPPVPDDCPTPLGVKKOKLPDSNEIVKLLRRKPIPDQGS 180
 Db 121 GYKSWFSFNSLSTYTBALPPVADGCPPLMGVKKKELPDSEIVKLLRRKPIPDQGT 180
 QY 181 NMMFAFAQHTHQPFTDKRGPAFTNGIGHVDLNIHGETLARQKRLRFRDGMKY 240
 Db 181 NMMFAFAQHTHQPFTDKRGPAFTNGIGHVDLNIHGETLARQKRLRFRDGMKY 240
 QY 241 QIIDGEMPEPTVADTOAEMITPPQVPEHLRFAVGQEVFGLVPGIMMYATITWLRHNK 300
 Db 241 QIINGEVIPTVADTOVEMITPPHPIRPHLRFAVGQEVFGLVPGIMMYATITWLRHNK 300
 QY 301 VLKQHPHWDGQLPQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDPPELLFNKQFOY 360
 Db 301 VLKQHPHWDGRLPQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDPPELLFNKQFOY 360
 QY 361 NRIIAEFNLLYHNPPLPTFOIHDQKNYQCIYNNSSILLEGITQFVASFTRQLAGRY 420
 Db 361 NRIIAEFNLLYHNPPLPTFOIHDQKNYQCIYNNSSILLEGITQFVASFTRQLAGRY 420
 QY 421 AGGRANVPAAVOKVQASIOSRQKQSFNRYKRFMLKPYSEFEELTGKESAELEAL 480
 Db 421 AGGRANVPAAVOKVQASIOSRQKQSFNRYKRFMLKPYSEFEELTGKESAELEAL 480
 QY 481 YGDIIDAVELLYPALVKEKPPDAIFGETVYVGAPELSKGLMGVNICSPAYMKPSTGGEV 540
 Db 481 YGDIIDAMELYPALVKEKPPDAIFGETVYVGAPELSKGLMGVNICSPAYMKPSTGGEV 540
 QY 541 GFOIINTASTIQSILCNVKGCPPTSGVPPPELTKVTYNASSSGGLDINPTVLKER 600
 Db 541 GFKIVNTASTIOSILCNVKGCPPTSGVPPPELTKVTYNASSSGGLDINPTVLKER 600
 QY 601 STEL 604
 Db 601 STEL 604

RESULT 4
 PGH2_BOVIN

ID PGH2 BOVIN STANDARD; PRT; 604 AA.
 AC 062698; 046517; 062665;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase
 -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2
 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).
 GN PGHS2 OR COX2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21141972; PubMed=11207216;
 RA Liu J., Antaya M., Goff A.K., Boerboom D., Silverides D.W.,
 RT Luster J.G., Stirois J.;
 RT "Molecular characterization of bovine prostaglandin G/H synthase-2 and
 regulation in uterine stromal cells.";
 RL Biol. Reprod. 64:983-991(2001).
 RN [2]
 RP SEQUENCE OF 105-253 FROM N.A.
 RX MEDLINE=98006431; PubMed=9348209;
 RA Asselin E., Drolet P., Fortier M.A.;
 RT "Cellular mechanisms involved during oxytocin-induced prostaglandin
 RT F2alpha production in endometrial epithelial cells in vitro: role of
 RT cyclooxygenase-2.";
 RL Endocrinology 138:4798-4805(1997).
 CC -1- FUNCTION: May have a role as a major mediator of inflammation
 and/or a role for prostanoid signaling in activity-dependent
 plasticity.
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
 H2 + A + H(2)O.
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
 molecule (By similarity).
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
 arachidonate; first step.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
 peroxidase.
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
 inflammatory drugs such as aspirin.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
 CC -----
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 use by non-profit institutions as long as its content is in no way
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AF031698; AAC04702.1; -;
 DR EMBL; AF031699; AAC28562.1; -;
 DR EMBL; AF004944; AAC05592.1; -;
 DR HSSP; Q05769; 1DDX.
 DR InterPro: IPR002007; Anim_peroxidase.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR002016; peroxidase.
 DR Pfam; PF03098; An_peroxidase; 1.
 DR PRINTS; PR00457; ANPEROXIDASE.
 DR SMART; SM00181; EGF_1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS50292; PEROXIDASE_3; 1.
 KW Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;

KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.
 FT SIGNAL 1 17
 FT CHAIN 18 604
 FT DOMAIN 18 55
 FT ACT SITE 193 193
 FT ACT SITE 371 371
 FT METAL 374 374
 FT SITE 516 516
 FT FT 21 32
 FT DISULFID 26 42
 FT DISULFID 44 54
 FT DISULFID 22 145
 FT DISULFID 555 561
 FT CONFLICT 6 6
 FT CONFLICT 111 111
 FT CONFLICT 458 458
 SQ SEQUENCE 604 AA; 65163 MW; 16EA2E51D0A01A45 CRC64;
 Query Match 90.3%; Score 2923; DB 1; Length 604;
 Best Local Similarity 88.9%; Pred. No. 1,3e-220; Indels 0; Gaps 0;
 Matches 537; Conservative 32; Mismatches 35;

QY 1 MLARALLCAVALALSHNTANPCSCSHPCQNRGVGVGFDPYKDCDCTRTGFYGENCSTPEFL 60
 DB 1 MLARALLCAVALALSGAANPCSCSHPCQNRGVGVGFDPYKDCDCTRTGFYGENCSTPEFL 60
 QY 61 TRIKLFIKPTNTHYILTHFGFNNVNNIPPLRNALSYVLTSRSHLIDSPPTYNADY 120
 DB 61 TRIKLFIKPTNTHYILTHFGFNNVNNIPPLRNALSYVLTSRSHLIDSPPTYNADY 120
 QY 121 GYKSWAENSLSYTRALPPVPDCCPTPLGVGKXQLPSNSIVETLLRKRFPDQGS 180
 DB 121 GYKSWAENSLSYTRALPPVPDCCPTPLGVGKXQLPSNSIVETLLRKRFPDQGS 180
 QY 121 SYKSWAENSLSYTRALPPVPDCCPTPLGVGKXQLPSNSIVETLLRKRFPDQGS 180
 DB 181 NMFAFFAQTHTQPFKTHKGRPAFTNGLGHVNLHYETLARORLRFKDGKMX 240
 DB 181 NMFAFFAQTHTQPFKTHKGRPAFTNGLGHVNLHYETLARORLRFKDGKMX 240
 QY 241 QIIDEMPPRYKDTQAEKTYIPPOVEHLRFVAVGEVGLVPLGMVATIMLRHNRYCD 300
 DB 241 QIIDEMPPRYKDTQAEKTYIPPOVEHLRFVAVGEVGLVPLGMVATIMLRHNRYCD 300
 QY 241 OMINEMPPRYKDTQAEKTYIPPOVEHLRFVAVGEVGLVPLGMVATIMLRHNRYCD 300
 DB 301 VLKQHPFPMGBOLEFQTSRLILIGETIKIVIEDYVOHLSGYNFKLKPDELLFNKQFOYQ 360
 DB 301 VLKQHPFPMGBOLEFQTSRLILIGETIKIVIEDYVOHLSGYNFKLKPDELLFNKQFOYQ 360
 QY 361 NRILAEFTLYHMHPLPDFTFOIHDQKYNQOIFYNNSILLEGITQFVESFTROLAGRV 420
 DB 361 NRILAEFTLYHMHPLPDFTFOIHDQKYNQOIFYNNSILLEGITQFVESFTROLAGRV 420
 QY 421 AGGRVNPVAVQVQASQSIDSRQMKYQSFNERRKFMKPYESEFELTGKEMSAELAL 480
 DB 421 AGGRVNPVAVQVQASQSIDSRQMKYQSFNERRKFMKPYESEFELTGKEMSAELAL 480
 QY 481 YGDIIDAVELYPALLVEKRPDAIFGETMVEGAPSLGMLGNVCSAYMKPSTFEGEV 540
 DB 481 YGDIIDAVELYPALLVEKRPDAIFGETMVEGAPSLGMLGNVCSAYMKPSTFEGEV 540
 QY 541 GFQIINTASIQSLICNNVKGCPFTSFVSPDELKTYVITNASSRSGHDDINPTYLKER 600
 DB 541 GFQIINTASIQSLICNNVKGCPFTSFVSPDELKTYVITNASSRSGHDDINPTYLKER 600
 QY 601 STEL 604
 DB 601 STEL 604

RESULT 5
 PGH2 CAVPO
 ID PGH2 CAVPO STANDARD; PRT; 604 AA.
 AC P70682;
 DT 01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase
 -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2
 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).
 PTGS2 OR COX2.
 OS Cavia porcellus (Guinea pig).
 CC Eukaryota; Metazoa; Chordata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriocognath; Cavidae; Cavia.
 CC NCBI_TaxID=10141;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=Hartley; TISSUE=Uterus;
 CC MEDLINE=97131952; PubMed=8977409;
 CC Bracken K.E., Elger W., Vanke I., Nanninga A., Gellersen B.;
 RT "Cloning of guinea pig cyclooxygenase-2 and 15-hydroxyprostaglandin
 RT dehydrogenase complementary deoxyribonucleic acids: steroid-modulated
 RT gene expression correlates to prostaglandin F2 alpha secretion in
 RT cultured endometrial cells.";
 CC Endocrinology 138:237-247(1997).
 CC -1- FUNCTION: May have a role as a major mediator of inflammation
 CC and/or a role for prostanoil signaling in activity-dependent
 CC plasticity.
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
 CC H2 + A + H(2)O.
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
 CC molecule (By similarity).
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
 CC arachidonate; first step.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
 CC peroxidase.
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
 CC inflammatory drugs such as aspirin.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: Y0786; CAA69204.1; -.
 CC HSSP: O05769; 1DDX.
 CC InterPro: IPR002007; AnlM_peroxidase.
 CC InterPro: IPR006209; EGF-like.
 CC InterPro: IPR006210; IEGF.
 CC InterPro: IPR002016; Peroxidase.
 CC Pfam: PF03098; An_peroxidase; 1.
 CC Pfam: PF00008; EGF; 1.
 CC PRINTS: PR00457; ANPEROXIDASE.
 CC SMART: SM00181; EGF; 1.
 CC PROSITE: PS00022; EGF_1; FALSE_NEG.
 CC PROSITE: PS01186; EGF_2; FALSE_NEG.
 CC PROSITE: PS50026; EGF_3; 1.
 CC OXidoreductase; Dioxygenase; Peroxidase; Glycoprotein;
 CC KM Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.
 CC SIGNL 1 17
 CC CHAIN 18 604
 CC DOMAIN 18 55
 CC ACT SITE 193 193
 CC ACT SITE 371 371
 CC METAL 374 374
 CC SITE 516 516
 CC DISULFID 21 32
 CC DISULFID 26 42
 CC DISULFID 44 54
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC BY SIMILARITY.

FT DISULFID 22 145 BY SIMILARITY.
 FT DISULFID 555 561 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 604 AA; 68883 MW; DA22ABD46ABFBBC5 CRC64;
 Query Match 89.3%; Score 2892; DB 1; Length 604;
 Best Local Similarity 87.3%; Pred. No. 3.5e-218;
 Matches 527; Conservative 44; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MLARALLCAVALISHTANPCSSHPQONRGVCMGVDFQKDCCTRTGYGNCSTPEFL 60
 DB 1 MLARALLCAVALISHTANPCSSHPQONRGVCMGVDFQKDCCTRTGYGNCSTPEFL 60
 QY 61 TRIKFLKPTNTVHYILTHFGFNNVNNIPFLNAMSIVLTSRSHISPPYNNADY 120
 DB 61 TRIKFLKPTNTVHYILTHFGFNNVNNIPFLNAMSIVLTSRSHISPPYNNADY 120
 QY 61 TRIKFLKPTNTVHYILTHFGFNNVNNIPFLNAMSIVLTSRSHISPPYNNADY 120
 DB 61 TRIKFLKPTNTVHYILTHFGFNNVNNIPFLNAMSIVLTSRSHISPPYNNADY 120
 QY 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVYKSKQLPDSNIEVKLLIRKFIIDPQGS 180
 DB 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVYKSKQLPDSNIEVKLLIRKFIIDPQGS 180
 QY 181 NMWFAFPAQHTFOFFKTDHKGPAFTNGLGHVDLNIYGETLAROKRLPFGOKMY 240
 DB 181 NMWFAFPAQHTFOFFKTDHKGPAFTNGLGHVDLNIYGETLAROKRLPFGOKMY 240
 QY 241 QITIDGMPPYTKDQOEMTYPPQVEHLRFVAGQVGLVGMVYATIMLRHNKVD 300
 DB 241 QITIDGMPPYTKDQOEMTYPPQVEHLRFVAGQVGLVGMVYATIMLRHNKVD 300
 QY 241 QITIDGMPPYTKDQOEMTYPPQVEHLRFVAGQVGLVGMVYATIMLRHNKVD 300
 DB 241 QITIDGMPPYTKDQOEMTYPPQVEHLRFVAGQVGLVGMVYATIMLRHNKVD 300
 QY 301 VLKQEPHWDRLPOTSRLLIGETIKIVIDYVQHLSGHFHKLFPDELLFNKQFOYQ 360
 DB 301 VLKQEPHWDRLPOTSRLLIGETIKIVIDYVQHLSGHFHKLFPDELLFNKQFOYQ 360
 QY 301 VLKQEPHWDRLPOTSRLLIGETIKIVIDYVQHLSGHFHKLFPDELLFNKQFOYQ 360
 DB 301 VLKQEPHWDRLPOTSRLLIGETIKIVIDYVQHLSGHFHKLFPDELLFNKQFOYQ 360
 QY 361 NRIAAEFTLYHMHPLPDTFOIHQKYNVQOFTYNNSTLLBHGTTQFVSEFTROLAGRY 420
 DB 361 NRIAAEFTLYHMHPLPDTFOIHQKYNVQOFTYNNSTLLBHGTTQFVSEFTROLAGRY 420
 QY 421 AGGRNPPAVQVQSASIDQSRQKQSFNEKRPMLKPYSPFEELTEKEMSAEEL 480
 DB 421 AGGRNPPAVQVQSASIDQSRQKQSFNEKRPMLKPYSPFEELTEKEMSAEEL 480
 QY 421 AGGRNPPAVQVQSASIDQSRQKQSFNEKRPMLKPYSPFEELTEKEMSAEEL 480
 DB 421 AGGRNPPAVQVQSASIDQSRQKQSFNEKRPMLKPYSPFEELTEKEMSAEEL 480
 QY 481 YGDIADVELYLPALVYKPRPDALFGETWVEGAPFSLKGLMGVNLCSPAYWKSTFGGEV 540
 DB 481 YGDIADVELYLPALVYKPRPDALFGETWVEGAPFSLKGLMGVNLCSPAYWKSTFGGEV 540
 QY 541 GFOIINTASIGSLICNNVKGCPETSFVDPBELIKVTYTNASSRSGLDINPTVLKER 600
 DB 541 GFOIINTASIGSLICNNVKGCPETSFVDPBELIKVTYTNASSRSGLDINPTVLKER 600
 QY 541 GFOIINTASIGSLICNNVKGCPETSFVDPBELIKVTYTNASSRSGLDINPTVLKER 600
 DB 541 GFOIINTASIGSLICNNVKGCPETSFVDPBELIKVTYTNASSRSGLDINPTVLKER 600
 QY 601 STEFL 604
 DB 601 STEFL 604
 QY 601 STEFL 604
 DB 601 STEFL 604
 RESULT 6
 PGH2_SHEEP STANDARD; PRT; 603 AA.
 AC P79208;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase
 -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2
 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).
 DE synchase 2) (PGH synthase 2) (PGHS-2) (PHS II).
 GN PTGS2 OR COX2.
 OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxID=9940;

[1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97032794; PubMed=8878543;
 RA Zhang V., O'Sullivan M., Hussain H., Roswit W.T., Holtzman M.J.;
 RT "Molecular cloning, functional expression, and selective regulation
 of ovine prostaglandin H synthase-2";
 RL Biochem. Biophys. Res. Commun. 227:499-506(1996).
 CC -1- FUNCTION: May have a role as a major mediator of inflammation
 and/or a role for prostanoic signaling in activity-dependent
 plasticity.
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
 H2 + A + H(2)O.
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
 molecule (by similarity).
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
 arachidonate, first step.
 CC -1- SUBUNIT: Homodimer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
 peroxidase.
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
 inflammatory drugs such as aspirin.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
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 or send an email to license@sdb-sdb.ch).

 DR EMBL: U68486; AAC48684.1; -.
 DR PIR: J05063; J05063.
 DR HSSP: Q05769; 3PGH.
 DR InterPro: IPR002007; Anim_peroxidase.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF03098; An_peroxidase; 1.
 DR Pfam: PF00008; EGF; 1.
 DR PRINTS: PRO0457; AMPEROXIDASE.
 DR SMART: SM00181; EGF; 1.
 DR PROSITE: PS00022; EGF_1; FALSE_NEG.
 DR PROSITE: PS01186; EGF_2; FALSE_NEG.
 DR PROSITE: PS50026; EGF_3; 1.
 DR PROSITE: PS50292; PEROXIDASE_3; 1.
 DR Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;
 KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.
 FT SIGNAL 1 16
 FT CHAIN 17 603
 FT DOMAIN 17 54
 FT ACT_SITE 192 192
 FT ACT_SITE 370 370
 FT METAL 373 373
 FT SITE 515 515
 FT DISULFID 20 31
 FT DISULFID 25 41
 FT DISULFID 43 53
 FT DISULFID 21 144
 FT DISULFID 554 560
 FT CARBOHYD 52 52
 FT CARBOHYD 129 129
 FT CARBOHYD 395 395
 FT CARBOHYD 579 579
 FT SEQUENCE 603 AA; 68969 MW; E27FE0549B81C52 CRC64;
 Query Match 89.0%; Score 2881.5; DB 1; Length 603;
 Best Local Similarity 87.6%; Pred. No. 2.3e-217;
 Matches 529; Conservative 35; Mismatches 39; Indels 1; Gaps 1;

QY 1 MLARALLICAVIALSHSTANPCSSHPQONRGVCSVGFQKDCDCTGTGEGNCSTPEEL 60
 Db 1 MLARALLICAVAVCG-AANPCSSHPQONRGVCSVGFQKDCDCTGTGEGNCSTPEEL 59
 QY 61 TRIKLFLKPTPTVHYILTHFGFNVVANNIPFLRNAISYVLTSRSHIDSPPTNADV 120
 Db 60 TRIKLFLKPTPTVHYILTHFGFNVVANNIPFLRNAISYVLTSRSHIDSPPTNADV 119
 QY 121 GKSWAEFNSLYTRALPPVDDCPTPLGVKQKQLPDSNIEVKKLRKRPDPQGS 180
 Db 120 GKSWAEFNSLYTRALPPVDDCPTPLGVKQKQLPDSNIEVKKLRKRPDPQGS 179
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 Db 180 NMMFAFPAQHFTHQFPEKTHKRGPAFTNGLGCVLNLHYGETLARGKRLFKQGMKY 239
 QY 241 QIIDEMYPPTVKDQIEMVTPPOVEHLRFVAVGQEVFGLVGLMMYATIMREHNRVD 300
 Db 240 QIIDEMYPPTVKDQIEMVTPPOVEHLRFVAVGQEVFGLVGLMMYATIMREHNRVD 299
 QY 301 VLKQHPPEWGEOLPQTSRLILIGETIKIVIEDVYQHLGSHYFKLPDELLFNQFOYQ 360
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 AC Q05769;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase
 -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2
 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II) (Glucocorticoid-
 DE regulated inflammatory cyclooxygenase) (Gripiphs) (TIS10 protein)
 DN (Macrophage activation-associated marker protein P71/73) (PES-2).
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss;
 RX MEDLINE=91302297; PubMed=1712772;
 RA Kujubu D.A., Fletcher B.S., Varnum B.C., Lim R.W., Herschman H.R.;
 RT "TIS10, a phorbol ester tumor promoter-inducible mRNA from Swiss 3T3
 cells, encodes a novel prostaglandin synthase/cyclooxygenase
 homologue".
 RU J. Biol. Chem. 266:12866-12872(1991).
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE=92165781; PubMed=1339449;
 RA Fletcher B.S., Kujubu D.A., Perrin D.M., Herschman H.R.;
 RT "Structure of the mitogen-inducible TIS10 gene and demonstration that
 RT the TIS10-encoded protein is a functional prostaglandin G/H
 RT synthase.";
 RL J. Biol. Chem. 267:4338-4344(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93041378; PubMed=1419907;
 RA Ryscek R.-P., Raynoschek C., Macdonald-Bravo H., Dorfman K.,
 RA Matrei M.-G., Bravo R.;
 RT "Identification of an immediate early gene, pghs-B, whose protein
 RT product has prostaglandin synthase/cyclooxygenase activity.";
 RL Cell Growth Differ. 3:443-450(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92279232; PubMed=1594589;
 RA O'Banion M.K., Mann V.D., Young D.A.;
 RT "cDNA cloning and functional activity of a glucocorticoid-regulated
 RT inflammatory cyclooxygenase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4888-4892(1992).
 RN [5]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=93246753; PubMed=8482922;
 RA Phillips T.A., Kujubu D.A., Mackay R.J., Herschman H.R., Russell S.W.,
 RA Pace J.L.;
 RT "The mouse macrophage activation-associated marker protein, p71/73,
 RT is an inducible prostaglandin endoperoxide synthase
 RT (cyclooxygenase).";
 RL J. Leukoc. Biol. 53:411-419(1993).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=9332648; PubMed=8349699;
 RA Otto J.C., Dewitt D.L., Smith W.L.;
 RT "N-glycosylation of prostaglandin endoperoxide synthases-1 and -2 and
 RT their orientations in the endoplasmic reticulum.";
 RL J. Biol. Chem. 268:18234-18242(1993).
 RN [7]
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 RX MEDLINE=97122334; PubMed=8967954;
 RA Kurnuball R.G., Stevens A.M., Gierse J.K., McDonald J.J.,
 RA Stegeman R.A., Pay J.Y., Gildenhau D., Miyashiro J.M., Penning T.D.,
 RA Seibert K., Isakson P.C., Stallings W.C.;
 RT "Structural basis for selective inhibition of cyclooxygenase-2 by
 RT anti-inflammatory agents.";
 RL Nature 384:644-648(1996).
 RN [8]
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 RA Kurnuball R.G., Stevens A.M., Gierse J.K., McDonald J.J.,
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 RA Seibert K., Isakson P.C., Stallings W.C.;
 RL Nature 385:555-555(1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.40 ANGSTROMS).
 RX MEDLINE=2026363; PubMed=10811226;
 RA Kiefer J.R., Pawlitz J.L., Moreland K.T., Stegeman R.A., Hood W.F.,
 RA Gierse J.K., Stevens A.M., Goodwin D.C., Rowlinson S.W., Marnett L.J.,
 RA Stallings W.C., Kurnuball R.G.;
 RT "Structural insights into the stereochemistry of the cyclooxygenase
 RT reaction.";
 RL Nature 405:97-101(2000).
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 RP FUNCTION: May have a role as a major mediator of inflammation
 RP and/or a role for prostanoil signaling in activity-dependent
 RP plasticity.
 RP -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
 RP H2 + A + H(2)O.
 RP -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
 RP molecule.
 RP -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
 RP arachidonate; first step.
 RP -1- SUBUNIT: Homodimer (by similarity).
 RP -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
 RP -1- INDUCTION: By cytokines and mitogens.

CC -1- MISCELLANEOUS: This enzyme acts both as a dioxigenase and as a
 CC peroxidase.
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
 CC inflammatory drugs such as aspirin.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
 CC -----
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 DR EMBL; M94967; AAA39918.1; -;
 DR EMBL; M82866; AAA40448.1; -;
 DR EMBL; M82862; AAA40448.1; JOINED.
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 DR EMBL; M82862; AAA37740.1; -;
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 DR PDB; 4COX; 24-DEC-97.
 DR PDB; 5COX; 24-DEC-97.
 DR PDB; 6COX; 24-DEC-97.
 DR PDB; 1CVU; 16-MAY-00.
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 DR PDB; 1DDX; 26-SEP-01.
 DR PDB; 1DDU; 26-SEP-01.
 DR GlycoSuiteDB; Q05769; -;
 DR MGD; MGI:97798; Pegs2.
 DR GO; GO:0005737; Cytoplasm; IDA.
 DR GO; GO:0008217; Regulation of blood pressure; IMP.
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 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PF03098; An_peroxidase; 1.
 DR Pfam; PF00008; EGF; 1.
 DR PRINTS; PR00457; ANPEROXIDASE.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS00022; EGF_1; FALSE NEG.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00262; PEROXIDASE_3; 1.
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 N-LINKED (GLCNAC. . .)
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FT CONFLICT 142 142 A -> R (IN REF. 3)
FT CONFLICT 585 585 H -> R (IN REF. 3)
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FT STRAND 28 29
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FT TURN 79 79
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FT TURN 90 90
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FT TURN 108 109
FT STRAND 116 117
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FT TURN 148 149

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Query Match Best Local Similarity 86.8%; Score 2873; DB 1; Length 604;
Matches 524; Conservative 39; Mismatches 41; Indels 0; Gaps 0;

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61 TRIKLLKPTNTVYIILTFKGFVNVNVIIFLNAMSYLTSRSHLIDSPPTYNADY
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181 NMMAFFPQHTHOFFKTDHKGPAFTNGLGVDLNIYGETLARQKRLFKDGKKY
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241 QIIGGEVPTVKQTQAEIYPPQVPELRAVGOEVLVGLMVAATIMLRHNRYCD
301 VLKQHPWGDQOLFQTSRLILIGTTIVIEDVYOHLSGHFKLKEPPELLFNKQFOYQ
301 VLKQHPWGDQOLFQTSRLILIGTTIVIEDVYOHLSGHFKLKEPPELLFNKQFOYQ
361 NRISAEPNTLYHMHPLPDFTENIEDQESFKQPLYNNSILHEGLITQVESFTQIAGR
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541 GFOINASTIOSLICNNVKGCPFTSVVPELKIYVINASSRSGLDINPTVLKRR
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Qy 601 STEL 604
Db 601 STEL 604

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AC P3535; 064379;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase
-2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2
synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).
GN PGH2 OR COX2 OR COX-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94092121; PubMed=791614;
RA Kennedy B.P., Chan C.C., Culp S.A., Cromlish W.A.;
RT "Cloning and expression of rat prostaglandin endoperoxide synthase
(cyclooxygenase)-2 cDNA.";
RL Biochem. Biophys. Res. Commun. 197;494-500(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93357029; PubMed=8352945;
RA Yamagata K., Andreasson K.I., Kaufmann W.E., Barnes C.A., Morley P.F.;
RT "Expression of a mitogen-inducible cyclooxygenase in brain neurons:
regulation by synaptic activity and glucocorticoids.";
RL Neuron 11;371-386(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Wistar; TISSUE=Intestine;
RA MEDLINE=94262786; PubMed=8203528;
RA Dubois R.N., Tsujii M., Bishop P., Awad J.A., Makita K.,
Lanahan A.;
RT "Cloning and characterization of a growth factor-inducible
cyclooxygenase gene from rat intestinal epithelial cells.";
RL Am. J. Physiol. 266;G822-G827(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=Fischer 344;
RA MEDLINE=94093619; PubMed=8274023;
RA Feng L., Sun W., Xia Y., Tang W.W., Channugam P., Soyoola E.,
Wilson C.B., Hwang D.;
RT "Cloning two isoforms of rat cyclooxygenase: differential regulation
of their expression.";
RL Arch. Biochem. Biophys. 307;361-368(1993).
CC -1- FUNCTION: May have a role as a major mediator of inflammation
and/or a role for prostanoind signaling in activity-dependent
plasticity.
CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
H2 + A + H(2)O.
CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
molecule (By similarity).
CC -1- PATHWAY: prostaglandins and thromboxanes biosynthesis from
arachidonate; first step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
populations of neurons and is enriched in the cortex and
hippocampus.
CC -1- INDUCTION: By cytokines and mitogens.
CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
peroxidase.
CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
inflammatory drugs such as aspirin.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.

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DR EMBL: U03389; AAA03466.1; -
DR EMBL: S67722; AAA29401.1; -
DR PIR: JC2030; JC2030.
DR HSSE: Q05769; 3PGH.
DR InterPro: IPR002007; Anim_peroxidase.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF03098; An_peroxidase; 1.
DR PRINTS: PR00457; ANPEROXIDASE.
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FT CHAIN 1 17
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Query Match 88.6%; Score 2866; DB 1; Length 604;
Best Local Similarity 86.4%; Pred. No. 2,7e-216;
Matches 522; Conservative 40; Mismatches 42; Indels 0; Gaps 0;

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QY 601 STEL 604
DB 601 STEL 604

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RESULT 9

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ID PGH2_MUSVI STANDARD; PRT; 604 AA.
AC 062725;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase
DE 2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2
DE synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).
GN PTGS2 OR COX2.
OS Mus musculus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=98344842; PubMed=9681517;
RA Song J.H., Stroids J., Houde A., Murphy B.D.;
RT "Cloning, developmental expression, and immunohistochemistry of
RT cyclooxygenase 2 in the endometrium during embryo implantation and
RT gestation in the mink (Mustela vison).";
RL Endocrinology 139:3629-3636(1998).
CC -1- FUNCTION: May have a role as a major mediator of inflammation
CC and/or a role for prostanoind signaling in activity-dependent
CC plasticity.
CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
CC H2 + A + H(2)O.
CC -1- COFACTOR: Binds 1 heme B (Iron-protoporphyrin IX) group per
CC molecule (By similarity).
CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
CC arachidonate, first step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
CC peroxidase.
CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
CC inflammatory drugs such as aspirin.
CC -1- SIMILARITY: Contains 1 EGF-like domain.

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AC	P27607;		
DT	01-AUG-1992 (Rel. 23, Created)		
DT	01-AUG-1992 (Rel. 23, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase		
DE	-2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2		
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OC	Gallus.		
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RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91187658; PubMed=1649272;		
RA	Xie W, Chipman J.G., Robertson D.L., Erikson R.L., Simmons D.L.;		
RT	"Expression of a mitogen-responsive gene encoding prostaglandin		
RT	synthase is regulated by mRNA splicing."		
RL	Proc. Natl. Acad. Sci. U.S.A. 88:2692-2696(1991).		
CC	-!- FUNCTION: May play an important role in regulating or promoting		
CC	cell proliferation in some normal and neoplastically transformed		
CC	cells.		
CC	-!- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin		
CC	H2 + A + H(2)O.		
CC	-!- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per		
CC	molecule (By similarity).		
CC	-!- PATHWAY: Prostaglandins and thromboxane biosynthesis from		
CC	arachidonate; first step.		
CC	-!- SUBUNIT: Homodimer (By similarity).		
CC	-!- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.		
CC	-!- INDUCTION: By cytokines and mitogens.		
CC	-!- MISCELLANEOUS: This enzyme acts both as a dioxxygenase and as a		
CC	peroxidase.		
CC	-!- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-		
CC	inflammatory drugs such as aspirin.		
CC	-!- SIMILARITY: Contains 1 EGF-like domain.		
CC	-!- SIMILARITY: Belongs to the prostaglandin G/H synthase family.		
CC	-----		
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CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.ebi.ac.uk/announcements		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; M64990; AAA49050.1; -		
OR	PIR; A38630; A38630.		

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DR HSPB; Q05769; 1CVU.
DR InterPro: IPR002007; Anim_peroxidase.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR002016; Peroxidase.
DR Pfam; PF03098; An_peroxidase; 1.
DR Pfam; PF00008; EGF; 1.
DR PRINTS; PR00457; ANPEROXIDASE.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50292; PEROXIDASE_3; 1.
DR Oxidoreductase; Dioxigenase; Glycoprotein;
  prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.
KW PROTAGLANDIN G/H SYNTHASE 2.
FT SIGNAL 1 17
FT CHAIN 18 603
FT DOMAIN 18 55
FT ACT_SITE 193 193
FT ACT_SITE 371 371
FT METAL 374 374
FT SITE 516 516
FT DISULFID 21 32
FT DISULFID 26 42
FT DISULFID 44 54
FT DISULFID 22 145
FT DISULFID 555 561
FT CARBOHYD 53 53
FT CARBOHYD 90 90
FT CARBOHYD 130 130
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FT SEQUENCE 603 AA; 69112 MW; BF0DFB3371189231 CRC64;

Query Match 84.2%; Score 2726.5; DB 1; Length 603;
Best Local Similarity 81.6%; Pred. No. 3e-205;
Matches 493; Conservative 56; Mismatches 54; Indels 1; Gaps 1;

1 MARALLICAVIALSTANPCSHPCQNGVCMVGDCPCPTGFGYGCSTPEFL 60
1 MLPCALMLAALAAAGANPCSLPCQNGVCMVGDCPCPTGFGYGCSTPEFL 60
61 TRIKLEKPTPTVHILTHFKGFNVNIPPLRNAINSVYLTSRSHLIDSPPTYNADY 120
61 TWIKLIKPTPTVHILTHFKGFNVNIPPLRNAINSVYLTSRSHLIDSPPTYNADY 120
121 GYKSWAFNSLSTYTRALPPVDDCTPIGVKCKKOLPDSNEVEKLLRKPIPPQGS 180
121 SYKSWAFNSLSTYTRALPPVDDCTPIGVKCKKOLPDSNEVEKLLRKPIPPQGS 180
181 NMWFAFQHFTHQFKTHKSGAPFNLGLGHGVDNLHLYGFTLAKQRLKFKDGMKY 240
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301 VLKQHPHEDDEQLFQTRILLIGETIKVIEYVQHLSGYHFKLKFDEPLLNQKFOY 360
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361 NRIAAEFNTLYHMHPLPDTFOIHDCKNYQCFYNNISILLEGITOFVESFTQIAG 420
361 NRIAAEFNTLYHMHPLPDTFOIHDCKNYQCFYNNISILLEGITOFVESFTQIAG 420
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421 AGGNVPAVQVQASIDSRQMKYQSFNEYRRRFLKPYSEFELTGEEKSAELAL 480
481 YGDIIDAVELPALIVEKRPDAITGEMVVEGAFSLKGLMGVNICSPAWKSGTGGEV 540
481 YGDIIDAVELPALIVEKRPDAITGEMVVEGAFSLKGLMGVNICSPAWKSGTGGEV 540
541 GPOIINNASQSLCNVKGCPFTSFVSPDELLKTVITINASSRSGLDINPTVLKER 600
541 GPOIINNASQSLCNVKGCPFTSFVSPDELLKTVITINASSRSGLDINPTVLKER 600

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Db 541 GPEIINNASQSLCNVKGCPFTSFVSPDELLKTVITINASSRSGLDINPTVLKER 599
QY 601 STEL 604
Db 600 SABL 603

RESULT 11
PGL1 HUMAN STANDARD; PRT; 599 AA.
ID PGL1 HUMAN Q15122;
AC P23219; Q15122;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Prostaglandin G/H synthase 1 precursor (EC 1.14.99.1) (Cyclooxygenase
-1) (COX-1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2
synthase 1) (PGH synthase 1) (PGHS-1) (PHS 1).
DE PTGS1 OR COX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_taxid=9606;
OX NCBI [1]
RN RP SEQUENCE FROM N.A.
RN RP MEDLINE=91317397; PubMed=1907252;
RN RX Funk C.D., Funk L.B., Kennedy M.E., Pong A.S., Fitzgerald G.A.;
RN RT "Human platelet/erythrocyte leukemia cell prostaglandin G/H synthase: cDNA
RN RT cloning, expression, and gene chromosomal assignment.";
RN RL FASEB J. 5:2304-2312(1991).
RN RN [2]
RN RP SEQUENCE FROM N.A.
RN RP TISSUE=Platelet;
RN RX MEDLINE=92134251; PubMed=1734857;
RN RA Takahashi Y., Ueda N., Yoshimoto T., Yamamoto S., Yokoyama C.,
RN RA Miyata A., Tanabe T., Fuse I., Hattori A., Shibata A.;
RN RT "Immunofluorescent purification and cDNA cloning of human platelet
RN RT prostaglandin endoperoxide synthase (cyclooxygenase).";
RN RL Biochem. Biophys. Res. Commun. 182:433-438(1992).
RN RN [3]
RN RP SEQUENCE FROM N.A.
RN RP TISSUE=Lung fibroblast;
RN RX MEDLINE=92268138; PubMed=1587858;
RN RA Diaz A., Reginaldo A.M., Jimenez S.A.;
RN RT "Alternative splicing of human prostaglandin G/H synthase mRNA and
RN RT evidence of differential regulation of the resulting transcripts by
RN RT transforming growth factor beta 1, interleukin 1 beta, and tumor
RN RT necrosis factor alpha.";
RN RL J. Biol. Chem. 267:10816-10822(1992).
RN RN [4]
RN RP SEQUENCE FROM N.A.
RN RP MEDLINE=90088508; PubMed=2512924;
RN RA Yokoyama C., Tanabe T.;
RN RT "Cloning of human gene encoding prostaglandin endoperoxide synthase
RN RT and primary structure of the enzyme.";
RN RL Biochem. Biophys. Res. Commun. 165:888-894(1989).
RN RN [5]
RN RP SEQUENCE FROM N.A., AND VARIANTS TRP-8 AND LEU-17.
RN RP Scott B.T., Haasstedt S.J., Bovill E.G., Callas P.W., Valliere J.E.,
RN RA Wang L.-H., Wu K.K., Long G.L.;
RN RT "Characterization of the human prostaglandin H synthase 1 gene
RN RT (PTGS1): exclusion by genetic linkage analysis as a second modifier
RN RT gene in familial thrombosis.";
RN RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN RN [6]
RN RP SEQUENCE FROM N.A. (ISOFORM LONG).
RN RP TISSUE=Brain;
RN RX MEDLINE=22388257; PubMed=12477932;
RN RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RN RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RN RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RN RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisler F.,
RN RA Diatchenko L., Marisano K., Farmer A.A., Rubin G.M., Hong L.,
RN RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKean P.J., McKean K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schenker A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences".
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play an important role in regulating or promoting
CC cell proliferation in some normal and neoplastically transformed
CC cells.
CC -!- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
CC H2 + A + H(2)O.
CC -!- COFACTOR: Binds heme B (iron-protoporphyrin IX) group per
CC molecule (by similarity).
CC -!- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
CC arachidonate; first step.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Membrane-associated. Mitochondrial membrane.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P23219-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P23219-2; Sequence=VSP_004673;
CC -!- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
CC peroxidase.
CC -!- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
CC inflammatory drugs such as aspirin.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
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CC EMBL: S36219; AAB22216.1; -;
CC EMBL: M59979; AAA03630.1; -;
CC EMBL: S36271; AAB22217.1; -;
CC EMBL: S78220; AAB21215.1; -;
CC EMBL: M31822; AAA36439.1; ALT. SEQ.
CC EMBL: M31812; AAA36439.1; JOINED.
CC EMBL: M31813; AAA36439.1; JOINED.
CC EMBL: M31815; AAA36439.1; JOINED.
CC EMBL: M31816; AAA36439.1; JOINED.
CC EMBL: M31817; AAA36439.1; JOINED.
CC EMBL: M31818; AAA36439.1; JOINED.
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CC EMBL: M31820; AAA36439.1; JOINED.
CC EMBL: M31821; AAA36439.1; JOINED.
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CC EMBL: BC029840; AAB29840.1; -;
CC PTR: JH0259; JH0259.
CC HSP: JH0259; JH0259.
CC Genew: HGNC:9604; PTGS1.
CC MIM: 176805; -;
CC GO: GO:0004666; F:prostaglandin-endoperoxide synthase activity; TAS.
CC GO: GO:0007582; P:physiological processes; TAS.
CC InterPro: IPR002007; Anim_peroxidase.
CC InterPro: IPR006209; EGF-like.
CC InterPro: IPR006210; IEGF.
CC InterPro: IPR02016; Peroxidase.

DR Pfam: PF03098; An_peroxidase; 1.
DR PRINTS: PR00457; ANPEROXIDASE.
DR SMART: SM00181; EGF_1.
DR PROSITE: PS00022; EGF_1; FALSE NEG.
DR PROSITE: PS01186; EGF_2; FALSE NEG.
DR PROSITE: PS50026; EGF_3; 1.
DR PROSITE: PS50292; PEROXIDASE_3; 1.
KW Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;
KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane;
KW EGF-like domain; Alternative splicing; Polymorphism.
FT SIGNAL 1 23
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FT DOMAIN 31 69
FT ACT SITE 206 206
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FT CARBOHYD 103 103
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FT VARIANT 8 8
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FT VARIANT 17 17
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FT VARIANT 359 359
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Best Local Similarity 59.9%; Pred. No.2.3e-151;
Matches 370; Conservative 94; Mismatches 120; Indels 34; Gaps 4;
QY 2 LARALLCAVATL-----SHTANPCSHPCQNRGVCMVGEPDYKDCCTR 46
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QY 47 TGFYGENCSTPEPLTRIKLFLKPTPNVHYILLTHKGVNVVNNIPFLRNALMSVYLSR 106
DB 61 TGYGPNCTIPGLMTWLNLSRPSFTFLHTRGMWEV-NATPIREMLMRLVITVR 119
QY 107 SHLIDSPPTVADYGYKSWEAFLSNLSYTRALPVPDDCPTPLGVKGGKOLPDSNEIVEK 166
DB 120 SNLIPSPPTVSADHYISWESFNSVSYTRILBSPVPCDCTPMTGKGGKOLPDAOLARR 179
QY 167 LLTRKRPIDPQSNMFAFPAGHFTHQFFKTDHKGPAFTNGLGAGVDLNIYGETLAR 226
DB 180 FLTRKRPIDPQSNMFAFPAGHFTHQFFKTSKMGKGFYKALGHVDLNIYGDNLER 239
QY 227 QRLRLFPDGMKQIIGDEMYRPTVKDQAEMLYRPQVPHRLFAVGQEFGLVGLMM 286
DB 240 QYQLRLFKDGLKQVLDGEMYPSPSEADVLMHYPRGIPQSGMAVGQEFGLVGLML 299
QY 287 YATLMREHNRVCDVLKQEHPEWGEDQLFQTSRLILGETIKYIETYDVVGLSGVHFLX 346
DB 300 YATLMREHNRVCDVLKQEHPEWGEDQLFQTSRLILGETIKYIETYDVVGLSGVHFLX 359
QY 347 FDEPLLNNKQFOYQNRILAAEENLTYHWHPLLPDFTQIHDQKXNYQGFYNNSLDEGIT 406
DB 360 FDEPLLFGVQFOYQNRILAAEENLTYHWHPLLPDFTQIHDQKXNYQGFYNNSLDEGIT 419

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 CC 586 --QDDGPVAV--ERPSTEL 599
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 CC RESULT 12
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 CC ID PGH1_RAT 063921; Q62731; Q63684;
 CC AC 15-DEC-1998 (Rel. 37, Last sequence update)
 CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Prostaglandin G/H synthase 1 precursor (EC 1.14.99.1) (Cyclooxygenase
 CC -1) (COX-1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2
 CC synthase 1) (PGH synthase 1) (PGHS-1) (PHS 1).
 CC GN PTGS1 OR COX1 OR COX-1.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_TaxId=10116;
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 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=Sprague-Dawley;
 CC RX MEDLINE=94099619; PubMed=8274023;
 CC RA Feng L., Sun W., Xia Y., Tang W.W., Channugam P., Soyoola E.,
 CC RA Wilson C.B., Hwang D.,
 CC RT "Cloning two isoforms of rat cyclooxygenase: differential regulation
 CC of their expression."
 CC RL Arch. Biochem. Biophys. 307:361-368(1993).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=Fischer 344; TISSUE=Trachea;
 CC RX MEDLINE=95168876; PubMed=7864644;
 CC RA Kitzler J., Hill E., Hardman R., Reddy N., Philpot R., Eling T.E.,
 CC RT "Analysis and quantitation of splicing variants of the TPA-inducible
 CC PGHS-1 mRNA in rat tracheal epithelial cells."
 CC RL Arch. Biochem. Biophys. 316:856-863(1995).
 CC CC -1- FUNCTION: May play an important role in regulating or promoting
 CC cell proliferation in some normal and neoplastically transformed
 CC cells.
 CC CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
 CC H2 + A + H(2)O.
 CC CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
 CC molecule (By similarity).
 CC CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
 CC arachidonate; first step.
 CC CC -1- SUBUNIT: Homodimer (By similarity).
 CC CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
 CC CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
 CC peroxidase.
 CC CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
 CC inflammatory drugs such as aspirin.
 CC CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
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 CC
 CC EMBL: U03388; AAA03465.1; -
 CC DR EMBL: S67721; AAB29400.2; -
 CC DR EMBL: U18060; AAA85823.1; -
 CC DR PIR: S69198; S69198.
 CC DR HSSP: P05979; ICOE.
 CC DR InterPro: IPR002007; Anm_peroxidase.
 CC DR InterPro: IPR006209; EGF_Like.
 CC DR InterPro: IPR006210; IEGF.
 CC DR InterPro: IPR02016; Peroxidase.
 CC DR Pfam: PF03098; An_peroxidase; 1.
 CC DR PRINTS: PR00457; ANPEROXIDASE.
 CC DR SMART: SM00181; EGF_1.
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 CC DR Oxidoreductase; Peroxidase; Glycoprotein;
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 CC Query Match 62.9%; Score 2036.5; DB 1; Length 602;
 CC Best Local Similarity 64.7%; Pred. No. 2,5e-151;
 CC Matches 357; Conservative 90; Mismatches 104; Indels 1; Gaps 1;
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 CC QY 19 NPCCSHPCQNRGVCMSYGFQDYKDCCTRTGFGYBNCSTPEFLIRIKLFLKPTPTVYIL 78
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 CC QY 79 TRKGFPNNVNNIPFLNAMSIVLTSRSHLDSPTTYNDYGYKSWEAFSNLSYTRAL 138
 CC DB TRKGFWIEFV-NATFLIREVIMRLVITRSNLISPPPTTYNAHDYISNESGNSVYTRIL 154
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 CC QY 139 PPVDDCPTPLGVGKQLPDSNEIVEKLIRKRPDPQGSNNMFAFPAQHTHOFPKT 198
 CC DB PSVKDDEPTMTGTSKQQLDPIHLAQRLLRRRIFIGPGQTNVLFAPFAQHTHOFPKT 214
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 CC QY 199 DKRGPAFTNGLGHVDLNIHGYETLARQRKLRFKQGXKXQIILIDEMNPPYKXDAE 258
 CC DB SKMGPGFTXALGHGVDLGHYDLSLRQYLLRFKQGXKXQYVLDGVRVPSVQASVL 274
 CC 215
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 CC 275

QY 319 RLIIIGETIKIVIEDVVOHLSGYNHFKLKPPELLFNKOFOYONRIAEFNTLYHMBLLP 378
 Db 335 RLIIIGETIKIVIEVVOHLSGYNHFKLKPPELLFNKOFOYONRIAEFNTLYHMBLLP 394
 QY 379 DTFOIHDOXKXNYOQFIYNNISILHEGITOFEVSEFTROIAGVAGGNVPAPVQVQASQ 438
 Db 395 DSFEVGSQEXSYEQFLFNTSMVDYGVVEALVDASRQAGRIIGGGRNFDYHVLHADV 454
 QY 439 DOSQOMKVSFNNYRKRFPMLKPYESPEELTGEKMSALEALYGDIDAVELYPALLVEKP 498
 Db 455 KESREMKLOSFEYERKRRFGKLPYTSFOEFTGEKEMAELELYGDIDALFFYGLMLEKC 514
 QY 499 RPDATFETWVEVGAFFSLKGLMGVNCSPAYKRPSTFGEVGFQIINTASISGLICNNY 558
 Db 515 QPNSLIGESMIEWGAFFSLKGLMGVNCSPAYKRPSTFGEVGFQIINTASISGLICNNY 574
 QY 559 KGCFTSFVSVD 570
 Db 575 KTCPVVSFRVPD 586

RESULT 13

PGH1_MOUSE STANDARD: PRT: 602 AA.

AC P22437;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Prostaglandin G/H synthase 1 precursor (EC 1.14.99.1) (Cyclooxygenase
 DE -1) (COX-1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2
 GN PTGS1 OR COX1 OR COX-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90203007; PubMed=2108169;
 RA Dewitt D.L., El-Hariri E.A., Kraemer S.A., Andrews M.J., Yao E.F.,
 RA Armstrong R.L., Smith W.L.;
 RT "The aspirin and heme-binding sites of ovine and murine prostaglandin
 RT endoperoxide synthases";
 RL J. Biol. Chem. 265:5192-5198(1990).
 CC -1- FUNCTION: May play an important role in regulating or promoting
 CC cell proliferation in some normal and neoplastically transformed
 CC cells.
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
 CC H2 + A + H(2)O.
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
 CC molecule (by similarity).
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
 CC arachidonate; first step.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
 CC peroxidase.
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
 CC inflammatory drugs such as aspirin.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, M4141; AAA39913.1; -.
 CC DR PIR; A35564; A35564.

DR HSSP; P05979; IDIY.
 DR MGD; MG1.97797; Ptgsl.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005792; C:mitosome; IDA.
 DR GO; GO:0001516; P:prostaglandin biosynthesis; IMP.
 DR GO; GO:0008217; P:regulation of blood pressure; IMP.
 DR InterPro; IPR002007; Anm peroxidase.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PF03098; An peroxidase; 1.
 DR PRINTS; PR00457; AMPEROXIDASE.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00262; EGF_3; 1.
 DR PROSITE; PS50292; PEROXIDASE_3; 1.
 DR Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;
 KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane;
 KM EGF-like domain.
 FT CHAIN 1..26
 FT DOMAIN 27..602
 FT ACT_SITE 209..209
 FT ACT_SITE 387..387
 FT METAL 390..390
 FT SITE 532
 FT DISULFID 38..49
 FT DISULFID 43..59
 FT DISULFID 61..71
 FT DISULFID 161
 FT DISULFID 571
 FT CARBOHYD 70
 FT CARBOHYD 106
 FT CARBOHYD 146
 FT CARBOHYD 146
 SQ SEQUENCE 602 AA; 69042 MW; 6340B602045C3A0 CRC64;

Query Match 62.6%; Score 2027.5; DB 1; Length 602;
 Best Local Similarity 65.0%; Pred. No. 1.3e-150;
 Matches 359; Conservative 86; Mismatches 106; Indels 1; Gaps 1;

QY 19 NPCCSHPCQNVGMSVGFDDYKCDPRTGYGNCSPPELTKLFLKPTNTVHTL 78
 Db 36 NPCCYPOQNGVCVRGLDNYQDCDCTRTGSGNCCTTPELWLRNSLRSPSTHLL 95
 QY 79 THFGFNVVNNIPLNAINSVYLTGRSHLIDSPYTNADYGYKSEAFNSLYTPAL 138
 Db 96 THGYWMEFV-NATFIREVIMRLVLTVRSNLIPSPPTYNASHDITSMESBSNVSYTRIL 154
 QY 139 PPVPDDCPPLGVYGVKKQLPDSNEIVKLLRRKFTIDPOGSMNMFAPAGHTHOPEKT 198
 Db 155 PSVXKDCPTPMGTGKQQLPDVOLLMOQLLRREFIPAPQGTNLLFAFPAQHFTHOPEKT 214
 QY 199 DHRKPAFTNGLSGVVDNHIYGETLARQKRLRFQGXKKYQVUIDEMPTPYKQDAE 258
 Db 215 SGKKGPFTALGHGVDLGHITYGDNLERQVHLRFQGXKKYQVUIDEVPVPSQASVL 274
 QY 259 MIYPPQVPELRAVGOEFGVGLMVAITMLREHNRVCDVLKQHPMGDEQLPOTS 318
 Db 275 MRYPGPVPPRQWAVGOEFGVGLPGLMFTIWLREHNRVCDLLKEHPMWDDEQLPOTT 334
 QY 319 RLIIIGETIKIVIEDVVOHLSGYNHFKLKPPELLFNKOFOYONRIAEFNTLYHMBLLP 378
 Db 335 RLIIIGETIKIVIEVVOHLSGYNHFKLKPPELLFNKOFOYONRIAEFNTLYHMBLLP 394
 QY 379 DTFOIHDOXKXNYOQFIYNNISILHEGITOFEVSEFTROIAGVAGGNVPAPVQVQASQ 438
 Db 395 DSFEVGSQEXSYEQFLFNTSMVDYGVVEALVDASRQAGRIIGGGRNFDYHVLHADV 454
 QY 439 DOSQOMKVSFNNYRKRFPMLKPYESPEELTGEKMSALEALYGDIDAVELYPALLVEKP 498
 Db 455 KESREMKLOSFEYERKRRFGKLPYTSFOEFTGEKEMAELELYGDIDALFFYGLMLEKC 514

QY 499 RPDALFETWVEGAPSLKLMGNVICSPEYKPTFGGVEGQIINTASIOSLICNNV 558
 Db 515 QPNSIFGSMTEMGAPSLKLMGNVICSPEYKPTFGGVEGQIINTASIOSLICNNV 574
 QY 559 KGCEPTSGSVDP 570
 Db 575 KTCFVSPRPD 586

RESULT 14
 PGH1_SHEEP
 ID PGH1_SHEEP STANDARD; PRT; 600 AA.
 AC P05379;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Prostaglandin G/H synthase 1 precursor (BC 1.14.99.1) (Cyclooxygenase
 -1) (COX-1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2
 synthase 1) (PGH synthase 1) (PGHS-1) (PHS 1).
 GN PGTSG1 OR COX1.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN (1)
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Vesicular gland;
 RX MEDLINE=88144447; PubMed=3125548;
 RA Dewitt D.L., Smith W.L.;
 RT "Primary structure of prostaglandin G/H synthase from sheep vesicular
 gland determined from the complementary DNA sequence.";
 RT Proc. Natl. Acad. Sci. U.S.A. 85:1412-1416(1988).
 RN (2)
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Vesicular gland;
 RX MEDLINE=88196421; PubMed=3129310;
 RA Yokoyama C., Takai T., Tanabe T.;
 RT "Primary structure of sheep prostaglandin endoperoxide synthase
 deduced from cDNA sequence.";
 RT FEBS Lett. 231:347-351(1988).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vesicular gland;
 RX MEDLINE=88153641; PubMed=2831188;
 RA Merlie J.P., Fagan D., Mudd J., Needleman P.;
 RT "Isolation and characterization of the complementary DNA for sheep
 seminal vesicle prostaglandin endoperoxide synthase
 (cyclooxygenase).";
 RT J. Biol. Chem. 263:3550-3553(1988).
 RN (4)
 RP SEQUENCE OF 523-544.
 RX MEDLINE=84024608; PubMed=6414516;
 RA Roth G.J., Machuga E.T., Ozols J.;
 RT "Isolation and covalent structure of the aspirin-modified,
 RT active-site region of prostaglandin synthetase.";
 RT Biochemistry 22:4672-4675(1983).
 RN (5)
 RP HEME-BINDING SITE.
 RX MEDLINE=90203007; PubMed=2108169;
 RA Dewitt D.L., El-Hariri E.A., Kraemer S.A., Andrews M.J., Yao E.F.,
 RA Armstrong R.L., Smith W.L.;
 RT "The aspirin and heme-binding sites of ovine and murine prostaglandin
 RT endoperoxide synthases.";
 RT J. Biol. Chem. 265:5192-5198(1990).
 RN (6)
 RP ACTIVE SITE TYR-385.
 RX MEDLINE=91056037; PubMed=2122967;
 RA Shimokawa T., Kilmacz R.J., Dewitt D.L., Smith W.L.;
 RT "Tyrosine 385 of prostaglandin endoperoxide synthase is required for
 RT cyclooxygenase catalysis.";
 RT J. Biol. Chem. 265:20073-20076(1990).
 RN (7)
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=93352648; PubMed=8349699;

RA Otto J.C., Dewitt D.L., Smith W.L.;
 RT "N-glycosylation of prostaglandin endoperoxide synthases-1 and -2 and
 RT their orientations in the endoplasmic reticulum.";
 RT J. Biol. Chem. 268:18234-18242(1993).
 RN (8)
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
 RX MEDLINE=94166877; PubMed=8121489;
 RA Picot D., Loll P.J., Garavito R.M.;
 RT "The X-ray crystal structure of the membrane protein prostaglandin H2
 RT synthase-1.";
 RT Nature 367:243-249(1994).
 RN (9)
 RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
 RX MEDLINE=96022982; PubMed=7552725;
 RA Loll P.J., Picot D., Garavito R.M.;
 RT "The structural basis of aspirin activity inferred from the crystal
 RT structure of inactivated prostaglandin H2 synthase.";
 RT Nat. Struct. Biol. 2:637-643(1995).
 RN (10)
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
 RX MEDLINE=96248328; PubMed=8652509;
 RA Loll P.J., Picot D., Ekabo O., Garavito R.M.;
 RT "Synthesis and use of iodinated antiinflammatory drug analogs as
 RT crystallographic probes of the prostaglandin H2 synthase
 RT cyclooxygenase active site.";
 RT Biochemistry 35:7330-7340(1996).
 RN (11)
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=20446270; PubMed=10988074;
 RA Malkowski M.G., Ginell S.L., Smith W.L., Garavito R.M.;
 RT "The productive conformation of arachidonic acid bound to
 RT prostaglandin synthase.";
 RT Science 289:1933-1937(2000).
 RN (12)
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=21167849; PubMed=1121413;
 RA Thureson E.D., Malkowski M.G., Lakkides K.M., Rieke C.J.,
 RA Mullichak A.M., Ginell S.L., Garavito R.M., Smith W.L.;
 RT "Mutational and X-ray crystallographic analysis of the interaction of
 RT dihydro-gamma-linolenic acid with prostaglandin endoperoxide H
 RT synthases.";
 RT J. Biol. Chem. 276:10358-10365(2001).
 RN (13)
 RP X-RAY CRYSTALLOGRAPHY (2.61 ANGSTROMS).
 RX MEDLINE=21218593; PubMed=11318639;
 RA Selinsky B.S., Gupta K., Sharkey C.T., Loll P.J.;
 RT "Structural analysis of NSAID binding by prostaglandin H2 synthase:
 RT time-dependent and time-independent inhibitors elicit identical enzyme
 RT conformations.";
 RT Biochemistry 40:5172-5180(2001).
 RL -1- FUNCTION: May play an important role in regulating or promoting
 CC cell proliferation in some normal and neoplastically transformed
 CC cells.
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
 CC H2 + A + H2O.
 CC -1- COFACTOR: Binds 1 heme B (Iron-protoporphyrin IX) group per
 CC molecule.
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
 CC arachidonate; first step.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. ENDOPLASMIC RETICULUM
 CC MEMBRANE AND MITOCHONDRIAL MEMBRANE.
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
 CC peroxidase.
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
 CC inflammatory drugs such as aspirin.
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
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DR EMBL: J03599; AAA31576.1; -
 DR EMBL: M18243; AAA31511.1; -
 DR EMBL: Y00750; CAA68719.1; -
 DR PIR: A28960; A28960.
 DR PIR: A29947; A29947.
 DR PDB: 1PRH; 31-MAR-95.
 DR PDB: 1PGE; 11-JAN-97.
 DR PDB: 1PGF; 11-JAN-97.
 DR PDB: 1PGG; 11-JAN-97.
 DR PDB: 1PTH; 11-APR-96.
 DR PDB: 1COE; 30-JUN-99.
 DR PDB: 1EBV; 20-FEB-02.
 DR PDB: 1IDY; 22-SEP-00.
 DR PDB: 1EOG; 09-MAY-01.
 DR PDB: 1E0H; 09-MAY-01.
 DR PDB: 1HTS; 27-JUN-01.
 DR PDB: 1HT8; 27-JUN-01.
 DR PDB: 1FE2; 02-MAY-01.
 DR PDB: 1IGX; 12-DEC-01.
 DR PDB: 1IGZ; 12-DEC-01.
 DR InterPro: IPR002007; Anni peroxidase.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF03098; An_peroxidase; 1.
 DR PRINTS: PR00457; ANPEROXIDASE.
 DR SMART: SM00181; EGF: 1.
 DR PROSITE: PS00022; EGF_1; FALSE_NEG.
 DR PROSITE: PS0186; EGF_2; FALSE_NEG.
 DR PROSITE: PS50026; EGF_3; 1.
 DR PROSITE: PS50292; PEROXIDASE_3; 1.
 DR Oxioreductase; Dioxigenase; Peroxidase; Glycoprotein;
 KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane;
 KW EGF-like domain; 3D-structure; Transmembrane.
 FT SIGNAL 1 24
 FT CHAIN 25 600 PROSTAGLANDIN G/H SYNTHASE 1.
 FT TRANSMEM 74 82
 FT TRANSMEM 86 92
 FT TRANSMEM 97 105
 FT TRANSMEM 108 122
 FT DOMAIN 32 70 EGF-LIKE.
 FT ACT_SITE 207 207 DIGITAL HISTIDINE.
 FT ACT_SITE 385 385 CYCLOOXYGENASE.
 FT METAL 388 388 IRON (HEME AXIAL LIGAND).
 FT SITE 530 530 ASPIRIN-ACETYLATED SERINE.
 FT DISULFID 36 47
 FT DISULFID 41 57
 FT DISULFID 59 69
 FT DISULFID 37 159
 FT DISULFID 569 575
 FT CARBOHYD 68 68
 FT CARBOHYD 144 144
 FT CARBOHYD 410 410
 FT VARIANT 97 97 N-LINKED (GLCNAC. . .)
 FT VARIANT 164 164 N-LINKED (GLCNAC. . .)
 FT VARIANT 456 456 R-LINKED (GLCNAC. . .)
 FT VARIANT 520 520 R -> H.
 FT VARIANT 525 525 R -> D.
 FT VARIANT 525 525 E -> Q OR K.
 FT MUTAGEN 385 385 M -> I.
 FT CONFLICT 1 3 Y->R; ABOLISHES CYCLOOXYGENASE ACTIVITY.
 FT CONFLICT 5 5 MSR -> MV (IN REF. 3).
 FT CONFLICT 5 5 S -> G (IN REF. 2).

Query Match 62.3%; Score 2016.5; DB 1; Length 600;
 Best Local Similarity 64.0%; Pred. No. 9.2e-150;
 Matches 354; Conservative 92; Mismatches 106; Indels 1; Gaps 1;

QY 19 NPCCSHPCQNRGVCMVSGFDQYKDCRTGTGFGSCSTPEFLFRILKFLKPTNTVHYIL 78
 QY 34 NPCCYPCQHQGICVAFGLBRYOCDCRRTYSGPNCITPEIWTITLRFSPSFTHML 93

QY 79 THEKGFNVNNIPIFLNALMSVYLFSSRLIDSPPTYNADYKSKMEAFNSLSYTRAL 138
 Db 94 THEKWLMDV-NATFIRDTLRLVLTFRSNLIPSPPTYNADHYISWESNSVSYTRIL 152
 QY 139 PVPDCCPTPLGVKVKKOLPDSNEIYKLLRRKFTPDQGSMMMAFPQOHTHOPEKT 198
 Db 153 PSVPRDCPTPMGTGKKOLPDAEFLRRRLRRKFTPDQGNLMFAFPQOHTHOPEKT 212
 QY 199 DHKGFPTNGLSGVLDLNIYGETLARQKTLRFQDKMKVOIIDGEMPTVKDTQAE 256
 Db 213 SGKMGFTKALGHVDLGHITGDNLEFRYQRLPFDGKUKTQMLNGEYVPSVEAPVL 272
 QY 259 MTPPVPEHLRFANGQEVFGLVPGIMVATTMLREHNVCDVLKQEHPEWGEOLFQTS 318
 Db 273 MAYPRGIPQSQMAVGQEVFGLPGIMVATTMLREHNVCDLKAHEHTWGEOLFQTA 332
 QY 319 RLILGETIKIYEDVVOHLSGYHFKLKDEPDLLENKQFOYQNRILAENTLYHMLLP 378
 Db 333 RLILGETIKIYEEVVOQLSGYFLQKFPDELLFGAOPQYRNRIAMENQULYHMLLP 392
 QY 379 DTFQIHDKYNYQCFIYNNSLLEHGIQFVESFTROIAGRVAGGRNPVAVQKVSQASI 438
 Db 393 DSFRVGPQDYSYEQFLFMTSMVDYGEALVDAPFGRQPRIGGGRNIDHILVAVDVI 452
 QY 439 DQSRQMKYQSPREYKREPMLEKYSFEELTGEKMSAELEALYGDIDAVELYPALLVEKP 498
 Db 453 KESRVLRLQPFNEYKRRKGRMKRYTSFOELTGEKMAAELEELYGDIDALEFPGILLEKC 512
 QY 499 RPDATFGEWVEGAPFSLKGLMGVICSPPYMKSTGEGEPQITNTASQSLCNV 558
 Db 513 HNSIFGSMLEMAPFSLKGLMGVICSPEYKASTGEGEWMVYVATLTKLVCIANT 572
 QY 559 KGCEFTSFVBDP 571
 Db 573 KTCFVPSFHVDP 585

RESULT 15
 PGH1_BOVIN STANDARD; PRT; 259 AA.
 AC 062664;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Prostaglandin G/H synthase 1 (EC 1.14.99.1) (Cyclooxygenase-1) (COX-1)
 DE 1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2 synthase 1) (PGH synthase 1) (PGHS-1) (PHS 1) (Fragment).
 DE 1) (PGH synthase 1) (PGHS-1) (PHS 1) (Fragment).
 GN PTGS1 OR COX1 OR COX-1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=98006431; PubMed=9348208;
 RA Aaseelin B., Drollet P., Fortier M.A.;
 RT "Cellular mechanisms involved during oxytocin-induced prostaglandin
 RT F2alpha production in endometrial epithelial cells in vitro: role of
 RT cyclooxygenase-2.";
 RL Endocrinology 138:4798-4805(1997).
 CC -!- FUNCTION: May play an important role in regulating or promoting
 CC cell proliferation in some normal and neoplastically transformed
 CC cells (By similarity).
 CC -!- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
 CC H2 + A + H(2)O.
 CC -!- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
 CC molecule (By similarity).
 CC -!- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
 CC arachidonate, first step.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.

CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
CC peroxidase.
CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal
CC anti-inflammatory drugs such as aspirin.
CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF004943; AAC05591.1; -.
DR HSSP; P05979; 1EQH.
DR InterPro; IPR002007; Anim peroxidase.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002016; Peroxidase.
DR Pfam; PF03098; An peroxidase; 1.
DR PRINTS; PR00457; ANPEROXIDASE.
DR PROSITE; PS50292; PEROXIDASE_3; 1.
KW Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;
KW Prostaglandin biosynthesis; Heme; Iron; Membrane.
FT NON TER 1 1
FT ACT SITE 87 87 DISTAL HISTIDINE (BY SIMILARITY).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON TER 259 259
SQ SEQUENCE 259 AA; 29830 MW; 6BE0D8C343C53F9E CRC64;

Query Match 31.0%; Score 1004; DB 1; Length 259;
Best Local Similarity 70.9%; Pred. No. 3.8e-71;
Matches 183; Conservative 30; Mismatches 45; Indels 0; Gaps 0;

QY 107 SHLIDSPPTYNADYGYKSWFAFSNLSYTRALPPVDDCPPLGVYKKGKQLPDSNEIVEK 166
Db 1 SNIIPSPPTYNVAHDYISWESFSNVSYSYTRILPSVPRDCPTPMGTGKKGQLPDAEFLSRR 60
QY 167 LILRRKFIIDPGGSNMMEFAFHQHTGQFFKTDHKGPAFTNGLGHGVDLNIHYETLAR 226
Db 61 FLIRRRKFIIDPGGSNMMEFAFHQHTGQFFKTDHKGPAFTNGLGHGVDLNIHYETLAR 120
QY 227 CRKRLRFKDGKMKYQIIDGEMYPPTVKDTQAEKIYPPQVBEHLRFVAGQEVFGLVPLMM 286
Db 121 RYQLRLFKDGKMKYQIIDGEMYPPTVKDTQAEKIYPPQVBEHLRFVAGQEVFGLVPLMM 180
QY 287 YATIWLRHNRYCDVLKQEHPEWDEQLFQTSRLIIGETIKIVIEDYVOHLSGYHFKLK 346
Db 181 YATIWLRHNRYCDVLKQEHPEWDEQLFQTSRLIIGETIKIVIEDYVOHLSGYHFKLK 240
QY 347 FDEBELLFNKQFOYQNRRIA 364
Db 241 FDEBELLFNKQFOYQNRRIA 258

Search completed: April 24, 2004, 07:19:43
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 24, 2004, 06:19:25 ; Search time 72 Seconds

(without alignments)
2646.847 Million cell updates/sec

Title: US-08-064-271-10

Sequence: 1 MARRALLCAVALSHSTANP.....RSGLDINPTVLLKERSTEL 604

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2967	91.7	604	6	Q8SPQ9
2	2949	91.1	604	6	Q8SPR3
3	2884	89.1	604	11	Q8VH41
4	2862	88.4	604	11	Q63124
5	2814	86.9	604	11	Q925V4
6	2606.5	80.5	561	11	Q7TMV2
7	2425	74.9	607	13	Q9PW89
8	2417	74.7	607	13	Q9W715
9	2331	72.0	601	13	Q8JH43
10	2198	67.9	449	6	Q9TJ26
11	2071.5	64.0	604	12	Q7TMB3
12	2047	63.2	422	6	Q9N288
13	2045.5	63.2	606	6	Q9N288
14	2041.5	63.0	593	13	Q8VUQ3
15	2040.5	63.0	597	13	Q8JH44
16	2029.5	62.7	633	6	Q8HZR1

17	2027.5	62.6	617	11	Q8CL16
18	2024.5	62.5	598	13	Q9PTN3
19	2013.5	62.2	624	13	Q9DEQ0
20	1769	54.6	339	4	Q81Z29
21	1584	48.9	589	5	Q9GPF4
22	1563	48.3	330	11	Q8CIP1
23	1540.5	47.6	592	5	Q96318
24	1047	32.3	414	6	Q8HZR0
25	905	28.0	178	6	Q9TVB3
26	844	26.1	164	11	Q8K3U5
27	842	26.0	178	11	Q7TQ43
28	779	24.1	202	11	Q7TQ44
29	734	22.7	204	6	Q9TT27
30	637	19.7	533	16	Q82V61
31	599	18.5	128	11	Q9WMH0
32	587	18.1	135	6	Q8WKE2
33	497	15.4	128	6	Q9N2C8
34	491	15.2	99	6	Q9BDG9
35	431	13.3	109	11	Q91ZN4
36	426	13.2	80	11	Q9QW72
37	299	9.2	92	13	Q9QW77
38	292	9.0	643	10	Q82031
39	289.5	8.9	99	6	Q9TS56
40	289	8.9	643	10	Q9AXU5
41	278	8.6	643	10	Q93X71
42	268.5	8.3	1432	5	Q18647
43	262.5	8.1	639	10	Q9SGH6
44	262.5	8.1	964	16	Q8ZMB6
45	254.5	7.9	1063	3	Q8X1B9

ALIGNMENTS

RESULT 1

Q8SPQ9 PRELIMINARY: FRT, 604 AA.

AC Q8SPQ9: 01-JUN-2002 (TRENBLREL. 21, Created)

DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)

DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)

DE Prostaglandin G/H synthase-2.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21850258; PubMed=11861541;

RA Boutemme D., Bouchard N., Boerboom D., Jones H.E., Goff A.K., Dore M., Stois J.

RT "Molecular Characterization of Canine Prostaglandin G/H Synthase-2 and Regulation in Prostatic Adenocarcinoma Cells in Vitro."

RL Endocrinology 143:1134-1143(2002).

DR EMBL: AY044905; AK97783.1; -

DR GO: GO:0004601; F:peroxidase activity; IEA.

DR GO: GO:0006979; P:response to oxidative stress; IEA.

DR InterPro: IPR002007; Anm_peroxidase.

DR InterPro: IPR006209; EGF_like.

DR InterPro: IPR006210; IEGF.

DR InterPro: IPR002016; Peroxidase.

DR Pfam: PF03098; An_peroxidase; 1.

DR Pfam: PF00008; EGF; 1.

DR PRINTS: PR00457; ANPEROXIDASE.

DR SMART: SM00181; EGF; 1.

DR PROSITE: PS50292; PEROXIDASE_3; 1.

SQ

SEQUENCE 604 AA; 68975 MW; 42CGFEH30DZB3928 CRC64;

Query Match 91.7%; Score 2967; DB 6; Length 604;

Best Local Similarity 90.1%; Pred. No. 1.6e-232;

Matches 544; Conservative 30; Mismatches 30; Indels 0; Gaps 0;

1 MARRALLCAVALSHSTANPCSHPCQNRGVGMSVGFQYKCDCTRTGFGYGCSTPEFL 60

Dr 1 MLEAALVYICAAIAVAVRAMPCSSHCCQOGICMSTGFDQYKDCDCTRTPYGENCSTPEFL 60

QY 61 TRIKLEFKPTNTYAHVILITHEKGFNNVANNIPELRNATMSYVLTSRSHLIDSPPTYNADY 120

Db 61 TRILKYLKPTNTYAHVILITHEKGFNNVANNIPELRNATIMKYVLTSRSHLIESPPTYNVY 120

QY 121 GYKSMWASNLSYYTRALRPVWDCCPTPLGYVKKKQLPDSNETVEKLLIRKRFITDPQGS 180

Db 121 GYKSMWASNLSYYTRALRPVWDCCPTPLGYVKKKQLPDSNETVEKLLIRKRFITDPQGS 180

QY 181 NMMPAFPEQHTHQFPTKDHKRGPAFTNGLGHGVDLNIHVEGTARQRRLRFKQKMKY 240

Db 181 NMMPAFPEQHTHQFPTKDHKRGPAFTNGLGHGVDLNIHVEGTARQRRLRFKQKMKY 240

QY 241 QIIGEMAPPEVCKDQAEMLYPPQVPEHLRFVAVGOEVEFGLVGLMMYATIMLREHNRVCD 300

Db 241 QVIDEAVLPPIVKDQVEMITYPNHPENHGFVAVGOEVEFGLVGLMMYATIMLREHNRVCD 300

QY 301 VLKQHPBPWGDQELFQTSRLILIGETIKIVIEDYVQHLSGYHFKKFDPELLFNQFOFQ 360

Db 301 VLKQHPBPWDEBRLFLQTSRLILIGETIKIVIEDYVQHLSGYHFKKFDPELLFNQFOFQ 360

QY 361 NRIAAEENTLYHMHLLPPTPIHQQKXVYQGFIVNNSLILHGLIQFESFPTQIAGRY 420

Db 361 NRIAAEENTLYHMHLLPPTPIHQQKXVYQGFIVNNSLILHGLIQFESFPTQIAGRY 420

QY 421 AGGRVVPVAVQVQASADISQSRQMYKQSFNEFRKRRLPYISFELLTEKEMAAGLEAL 480

Db 421 AGGRVVPVAVQVQASADISQSRQMYKQSFNEFRKRRLPYISFELLTEKEMAAGLEAL 480

QY 481 YGDIDAVELYPALLVEKRPDPAIFGETWVEVGAPESLKGLGMNVICSPAYWKSSTGGEV 540

Db 481 YGDIDAVELYPALLVEKRPDPAIFGETWVEVGAPESLKGLGMNVICSPAYWKSSTGGEV 540

QY 541 GQIINTASTISLICNNVNGCPTTSVDPDELKIVTINASSRSGLDINPTVLKER 600

Db 541 GKRIINTASTISLICNNVNGCPTTAVSDQGLTKIVTINASSRSGLDINPTVLKER 600

QY 601 STEL 604

Db 601 STEL 604

RESULT 2

Q8SPR3 PRELIMINARY; PRT; 604 AA.

ID Q8SPR3

AC Q8SPR3; 01-JUN-2002 (TEMBLrel. 21, Created)

DT 01-JUN-2002 (TEMBLrel. 21, last sequence update)

DT 01-OCT-2003 (TEMBLrel. 25, last annotation update)

DE Prostaglandin G/H synthase-2.

GN PGHS-2.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxId=9823;

RN

RP SEQUENCE FROM N.A.

RA LaJote S., Stoids J., Dore M.;

RT "Expression of Cyclooxygenase-2 in Naturally-Occurring Porcine Gastric Ulcers."

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY028583; AAK27263.1; -

DR GO; GO:0004601; F:peroxidase activity; IEA.

DR GO; GO:0006979; P:response to oxidative stress; IEA.

DR InterPro; IPRO02007; Anim_peroxidase.

DR InterPro; IPRO06209; EGF like.

DR InterPro; IPRO06210; IEGF.

DR InterPro; IPRO02016; peroxidase.

DR Pfam; PF03098; An_peroxidase; 1.

DR Pfam; PF00008; EGF; 1.

DR PRINTS; PR00457; ANPEROXIDASE.

DR	SMART; SM00181; EGF_1;
DR	PROSITE; PS50292; PPKOXIDASE_3; 1.
SEQUENCE	604 AA; 69145 MW; DA951E35205F9A90 CRC64;
Query Match	91.1%; Score 2949; DB 6; Length 604;
Best Local Similarity	89.6%; Pred. No. 4.6e-21;
Matches 541; Conservative	28; Mismatches 33; Indels 0; Gaps 0;

QY	1	MLABALLICAVLALISHTANPCCSHPCONRGVCMVGFOYKCDCTRTGFGYBNCSTPEFL	60
QY	1	MLABALLICAVLALISHTANPCCSHPCONRGVCMVGFOYKCDCTRTGFGYBNCSTPEFL	60
Db	1	MLABALLICAVLALISHTANPCCSHPCONRGVCMVGFOYKCDCTRTGFGYBNCSTPEFL	60
QY	61	TRIKLFLKPTNTVHYILLTHEKGFNNVNNNIPPLRNATMSVLNRSRHLIDSPPTVANDY	120
Db	61	TRIKLFLKPTNTVHYILLTHEKGFNNVNNNIPPLRNATMSVLNRSRHLIDSPPTVANDY	120
QY	121	GYSKWEAFNSLSYTRALPVPDDCPFLDGYKKQKOLDSNEIYEKULLRRKFLPDQGS	180
Db	121	GYSKWEAFNSLSYTRALPVPDDCPFLDGYKKQKOLDSNEIYEKULLRRKFLPDQGS	180
QY	181	NMGEAFPAQHFTHOFKFTDHRKGRPAFTNGLGHGVNLNIYEBTLAROKRLRFKQGMKY	240
Db	181	NMGEAFPAQHFTHOFKFTDHRKGRPAFTNGLGHGVNLNIYEBTLAROKRLRFKQGMKY	240
QY	241	QIIDSEMPPTVKDQAEIMYPPQVPEHLREAVQGEVGLVGLMAYATIMLRHNRYCD	300
Db	241	QIIDSEMPPTVKDQAEIMYPPQVPEHLREAVQGEVGLVGLMAYATIMLRHNRYCD	300
QY	301	VLKQHPHPCWGEOLFOYSRLILIGETIKIVIEDYVOHLSGYHFKLEDPBELLFNKQFOYO	360
Db	301	VLKQHPHPCWGEOLFOYSRLILIGETIKIVIEDYVOHLSGYHFKLEDPBELLFNKQFOYO	360
QY	361	NRIAAEFTLLYMHMLPPTPOIHQKXNYOOFIANNLSLHGTQFVESPTROLAGRY	420
Db	361	NRIAAEFTLLYMHMLPPTPOIHQKXNYOOFIANNLSLHGTQFVESPTROLAGRY	420
QY	421	AGGRAVPPAVQVQSASIDQSRQMKYQSFNEFRKGFMLKPYSPFELTGKEMSALEAL	480
Db	421	AGGRAVPPAVQVQSASIDQSRQMKYQSFNEFRKGFMLKPYSPFELTGKEMSALEAL	480
QY	481	YGDIDAVELYPALLVEKPRPDAIFGRTMYEVGAPFSLKGLMGNVICSPEYKRPSTGGEV	540
Db	481	YGDIDAVELYPALLVEKPRPDAIFGRTMYEVGAPFSLKGLMGNVICSPEYKRPSTGGEV	540
QY	541	GROITNTASTQSLCNVNGKGCPTSGVDPDELKIVTINASSRGLDINDPTVLKER	600
Db	541	GROITNTASTQSLCNVNGKGCPTSGVDPDELKIVTINASSRGLDINDPTVLKER	600
QY	601	STEL 604	
Db	601	STEL 604	
RESULT 3			
Q8VH41			
ID	Q8VH41	PRELIMINARY;	PRT; 604 AA.
AC	Q8VH41		
DT	01-MAR-2002	(TEMBLrel. 20, Created)	
DT	01-MAR-2002	(TEMBLrel. 20, last sequence update)	
DT	01-OCT-2003	(TEMBLrel. 25, last annotation update)	
DE	Prostaglandin H synthase 2.		
GN	COX2.		
OS	Sigmodon hispidus (Hispid cotton rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;		
OC	Sigmodon.		
OX	NCBI_TaxID=42415;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Blanco J.C., Pletneva L.M., Prince G.A.;		
RT	"Sigmodon hispidus cytokines", chemokines and interferons."		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY065644; AAL55393.1; -.		

DR GO: 0004601; F: peroxidase activity; IEA.
 DR GO: 0006979; P: response to oxidative stress; IEA.
 DR InterPro: IPR002007; AnIm_peroxidase.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF03098; An_peroxidase; 1.
 DR PRINTS: PR00457; ANPEROXIDASE.
 DR SMART: SM00181; EGF; 1.
 DR PROSITE: PS50292; PEROXIDASE_3; 1.
 DR SEQUENCE 604 AA; 69084 MW; 3B4A416A5F33BAC1 CRC64;

Query Match 89.1%; Score 2884; DB 11; Length 604;
 Best Local Similarity 87.1%; Pred. No. 8.9e-226;
 Matches 526; Conservative 39; Mismatches 39; Indels 0; Gaps 0;

QY 1 M LARALLLCALVALSHTANPCSSHPCONRGVMSVGFQYKCDCTRTGFGENCSTPEFL 60
 DB 1 M LFRVAVLICALALSHANPCSNPCONRGECMTVGFQYKCDCTRTGFGENCCTPEFL 60
 QY 61 TRIKLFLKPTNTVHIIITHFKGFVNVNIIPLRLNALSIVLTSSHLIDSPTYNADY 120
 DB 61 TRIKLFLKPTNTVHIIITHFKGFVNVNIIPLRLSIRMYVLTSSHLIDSPTYNVH 120
 QY 121 GYKSWAFSNLSYTTALPVPDDCPTPLGVKSKQQLPSNNEIVEKLLRRKTIPOGGS 180
 DB 121 GYKSWAFSNLSYTTALPVPDDCPTPLGVKSKKELPSKEVLEKVLRRKEIPDOGT 180
 QY 181 NMFAFAFHQFTHQFETDHRKGPFTNGIGHGVDLNHYGETLAROKRLFKDGKMKY 240
 DB 181 NMFAFAFHQFTHQFETDHRKGPFTNGIGHGVDLNHYGETLDHOKRLFKDGKMKY 240
 QY 241 QIIDGMYPPTVKOTQAEIMTYPPQVEHLRFVAGQEVFGVPGIMMYATITWREHNRVCD 300
 DB 241 QVIDGEVYPTVKOTQVEMITPPHIEHLRFVAGQEVFGVPGIMMYATITWREHNRVCD 300
 QY 301 VLKQHPENDDELFQTSRLILGETIKIVIEDYVQHLSGYHFKLKFDELLFNQOFQY 360
 DB 301 VLKQHPENDDELFQTSRLILGETIKIVIEDYVQHLSGYHFKLKFDELLFNQOFQY 360
 QY 361 NRIASEFNTLYHMHPLPDTFOIHQKYNVQCFIYNNSTILBHGITOQVESFTROIAGRV 420
 DB 361 NRIASEFNTLYHMHPLPDTFOIJDQKYNVQCFIYNNSTILBHGITHFVESFTROIAGRV 420
 QY 421 AGGRNVPRVQVQSASIDQSRQMKYQSFNEVYKRFMLKPYSPFEELTEKEMASLEAL 480
 DB 421 AGGRNVPRVQVQSASIDQSRQMKYQSFNEVYKRFMLKPYSPFEELTEKEMASLEAL 480
 QY 481 YGDIIDAVELYPALVLEKRPDAIFGETMVEGAPFSLKGLMGNVICSPPYMKRSTFGGV 540
 DB 481 YNDIDAMELYPALVLEKRPDAIFGETMVEGAPFSLKGLMGNPICSPPYMKRSTFGGV 540
 QY 541 GFQIINTASIQSLICNNVGCPTSPSVDPDELIKVTINASSRSGLDINDPTVLLKER 600
 DB 541 GFRIINTASIQSLICNNVGCPTSPSVDPDELIKVTINASSRSGLDINDPTVLLKER 600
 QY 601 STEL 604
 DB 601 STEL 604
 RESULT 4
 ID Q63124 PRELIMINARY; PRT; 604 AA.
 AC Q63124;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Cyclooxxygenase-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
 RA Yamagata K.K.Y.;
 RT "Expression of a mitogen-inducible cyclooxxygenase in brain neurons:
 RT Regulation by synaptic activity and glucocorticoids."
 RL Neuron 0:0-0(1993).
 DR EMBL; L20085; AAA40947.1; -.
 DR HSSP; Q05769; 1DDX.
 DR GO: 0004601; F: peroxidase activity; IEA.
 DR GO: 0006979; P: response to oxidative stress; IEA.
 DR InterPro: IPR002007; AnIm_peroxidase.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF03098; An_peroxidase; 1.
 DR PRINTS: PR00457; ANPEROXIDASE.
 DR SMART: SM00181; EGF; 1.
 DR PROSITE: PS50292; PEROXIDASE_3; 1.
 DR SEQUENCE 604 AA; 69130 MW; 98E7BB71080E6F0C CRC64;

Query Match 88.4%; Score 2862; DB 11; Length 604;
 Best Local Similarity 86.3%; Pred. No. 5.5e-224;
 Matches 521; Conservative 40; Mismatches 43; Indels 0; Gaps 0;

QY 1 M LARALLLCALVALSHTANPCSSHPCONRGVMSVGFQYKCDCTRTGFGENCSTPEFL 60
 DB 1 M LFRVAVLICALALSHANPCSNPCONRGECMTVGFQYKCDCTRTGFGENCCTPEFL 60
 QY 61 TRIKLFLKPTNTVHIIITHFKGFVNVNIIPLRLNALSIVLTSSHLIDSPTYNADY 120
 DB 61 TRIKLFLKPTNTVHIIITHFKGFVNVNIIPLRLSIRMYVLTSSHLIDSPTYNVH 120
 QY 121 GYKSWAFSNLSYTTALPVPDDCPTPLGVKSKQQLPSNNEIVEKLLRRKTIPOGGS 180
 DB 121 GYKSWAFSNLSYTTALPVPDDCPTPLGVKSKKELPSKEVLEKVLRRKEIPDOGT 180
 QY 181 NMFAFAFHQFTHQFETDHRKGPFTNGIGHGVDLNHYGETLAROKRLFKDGKMKY 240
 DB 181 NMFAFAFHQFTHQFETDHRKGPFTNGIGHGVDLNHYGETLDHOKRLFKDGKMKY 240
 QY 241 QIIDGMYPPTVKOTQAEIMTYPPQVEHLRFVAGQEVFGVPGIMMYATITWREHNRVCD 300
 DB 241 QVIDGEVYPTVKOTQVEMITPPHIEHLRFVAGQEVFGVPGIMMYATITWREHNRVCD 300
 QY 301 VLKQHPENDDELFQTSRLILGETIKIVIEDYVQHLSGYHFKLKFDELLFNQOFQY 360
 DB 301 VLKQHPENDDELFQTSRLILGETIKIVIEDYVQHLSGYHFKLKFDELLFNQOFQY 360
 QY 361 NRIASEFNTLYHMHPLPDTFOIHQKYNVQCFIYNNSTILBHGITOQVESFTROIAGRV 420
 DB 361 NRIASEFNTLYHMHPLPDTFNIJDQKYNVQCFIYNNSTILBHGITHFVESFTROIAGRV 420
 QY 421 AGGRNVPRVQVQSASIDQSRQMKYQSFNEVYKRFMLKPYSPFEELTEKEMASLEAL 480
 DB 421 AGGRNVPRVQVQSASIDQSRQMKYQSFNEVYKRFMLKPYSPFEELTEKEMASLEAL 480
 QY 481 YGDIIDAVELYPALVLEKRPDAIFGETMVEGAPFSLKGLMGNVICSPPYMKRSTFGGV 540
 DB 481 YNDIDAMELYPALVLEKRPDAIFGETMVEGAPFSLKGLMGNPICSPPYMKRSTFGGV 540
 QY 541 GFQIINTASIQSLICNNVGCPTSPSVDPDELIKVTINASSRSGLDINDPTVLLKER 600
 DB 541 GFRIINTASIQSLICNNVGCPTSPSVDPDELIKVTINASSRSGLDINDPTVLLKER 600
 QY 601 STEL 604
 DB 601 STEL 604

RESULT 5
 ID Q925V4 PRELIMINARY; PRT; 604 AA.
 AC Q925V4;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (Trembl. 19, last sequence update)
 DT 01-OCT-2003 (Trembl. 25, last annotation update)
 DE Cyclooxygenase-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20390055; PubMed=10816563;
 RA Xu K., Robida A.M., Murphy T.J.;
 RT "Immediate-early MEK-1-dependent Stabilization of Rat Smooth Muscle
 Cell Cyclooxygenase-2 mRNA by G-protein-coupled Receptor Signaling.";
 RL J Biol. Chem. 275:23012-23019(2000).
 DR EMBL: AF233596; AAF36986.1; -
 DR GO: GO:0004601; Peroxidase activity; IEA.
 DR GO: GO:0006979; Response to oxidative stress; IEA.
 DR InterPro: IPR002007; Anion peroxidase.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF03098; An. peroxidase; 1.
 DR PRINTS: PR00457; ANPEROXIDASE.
 DR PROSITE: PS50292; PEROXIDASE_3; 1.
 SQ SEQUENCE 604 AA; 69234 MW; 3FBD4E73FF4965F CRC64;
 Query Match 86.9%; Score 2814; DB 11; Length 604;
 Best Local Similarity 84.9%; Pred. No. 4.4e-220;
 Matches 513; Conservative 41; Mismatches 50; Indels 0; Gaps 0;

QY 1 MLRALILCAVALLSHTANPCSHPCNRCVCSVGFQYKCDCTRGTGFGNCSTPEFL 60
 Db 1 MLRAVILCALGPGSHANPCSCNRCGECMSIGDQYKCDCTRGTGFGNCSTPEFL 60

QY 61 TRIKFLKPTPNVTHYLTHFGKGMVNNIPLRLNAINSVLTSTRSHLIDSEPTVADY 120
 Db 61 TRIKFLKPTPNVTHYLTHFGKGMVNNIPLRLNAINSVLTSTRSHLIDSEPTVADY 120

QY 121 GYSWMEFSLSYSTRALPEVPDDCPTPLGVKGGKOLPDSNEIYEKLLRRKFLPDPQGS 180
 Db 121 GYSWMEFSLSYSTRALPEVPDDCPTPLGVKGGKOLPDSNEIYEKLLRRKFLPDPQGS 180

QY 181 NMWFAFPAQHTHOFKTDHKGPAFTNGLGHVLDNHYGETLARQKRLFPDGMKY 240
 Db 181 NMWFAFPAQHTHOFKTDHKGPAFTNGLGHVLDNHYGETLARQKRLFPDGMKY 240

QY 241 QIIDGEMVPTVADTQEMTYPPOVPEHLRPAVQEVGLVPGIMATYTLRHNHVC 300
 Db 241 QIIDGEMVPTVADTQEMTYPPOVPEHLRPAVQEVGLVPGIMATYTLRHNHVC 300

QY 301 VLKQEHFEMWDEQLFQTSRLILIGETIKIYIEDVYVGHLSGHNFLKRPDELLFNKQFOYQ 360
 Db 301 VLKQEHFEMWDEQLFQTSRLILIGETIKIYIEDVYVGHLSGHNFLKRPDELLFNKQFOYQ 360

QY 361 NRIAEFNTLYHMHPLLPDTFQIHDKQKXNQOFLYNNSSILHEGITOVSFTRQAGRY 420
 Db 361 NRIAEFNTLYHMHPLLPDTFQIHDKQKXNQOFLYNNSSILHEGITOVSFTRQAGRY 420

QY 421 AGGNVPAVQKYSQASIDSRQKQYSPNEYRRKRPFLKPESEETLGEKEMAELEAL 480
 Db 421 AGGNVPAVQKYSQASIDSRQKQYSPNEYRRKRPFLKPESEETLGEKEMAELEAL 480

QY 481 YGIDDAVEIYVALLVERPRDAIFGETMVEVGAFFSLKGLMGNVIGSPAYWKESTFGGEV 540
 Db 481 YGIDDAVEIYVALLVERPRDAIFGETMVEVGAFFSLKGLMGNVIGSPAYWKESTFGGEV 540

QY 541 GFOIINTASIQSLICNNVKGCPFTSFVDPBELIKVTINASSRSGLDINPTVLKER 600
 Db 541 GFOIINTASIQSLICNNVKGCPFTSFVDPBELIKVTINASSRSGLDINPTVLKER 600

QY 601 STEL 604
 Db 601 STEL 604

RESULT 6
 Q7TW2 PRELIMINARY; PRT; 561 AA.
 ID Q7TW2;
 AC Q7TW2;
 DT 01-OCT-2003 (Trembl. 25, Created)
 DT 01-OCT-2003 (Trembl. 25, last sequence update)
 DT 01-OCT-2003 (Trembl. 25, last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/He; TISSUE=Mesenchymal Stem Cell;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettelman M., Madan A., Kodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Klausner R.D., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/He; TISSUE=Mesenchymal Stem Cell;
 RX Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC052900; AAH52900.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 561 AA; 63857 MW; 1CC5F645AD6738B5 CRC64;
 Query Match 80.5%; Score 2606.5; DB 11; Length 561;
 Best Local Similarity 79.5%; Pred. No. 3e-203;
 Matches 480; Conservative 39; Mismatches 42; Indels 43; Gaps 1;

QY 1 MLRALILCAVALLSHTANPCSHPCNRCVCSVGFQYKCDCTRGTGFGNCSTPEFL 60
 Db 1 MLRAVILCALGPGSHANPCSCNRCGECMSIGDQYKCDCTRGTGFGNCSTPEFL 60

QY 61 TRIKFLKPTPNVTHYLTHFGKGMVNNIPLRLNAINSVLTSTRSHLIDSEPTVADY 120
 Db 61 TRIKFLKPTPNVTHYLTHFGKGMVNNIPLRLNAINSVLTSTRSHLIDSEPTVADY 120

QY 121 GYSWMEFSLSYSTRALPEVPDDCPTPLGVKGGKOLPDSNEIYEKLLRRKFLPDPQGS 180
 Db 121 GYSWMEFSLSYSTRALPEVPDDCPTPLGVKGGKOLPDSNEIYEKLLRRKFLPDPQGS 180

QY 181 NMWFAFPAQHTHOFKTDHKGPAFTNGLGHVLDNHYGETLARQKRLFPDGMKY 240
 Db 181 NMWFAFPAQHTHOFKTDHKGPAFTNGLGHVLDNHYGETLARQKRLFPDGMKY 240

QY 241 QIIDGEMVPTVADTQEMTYPPOVPEHLRPAVQEVGLVPGIMATYTLRHNHVC 300
 Db 241 QIIDGEMVPTVADTQEMTYPPOVPEHLRPAVQEVGLVPGIMATYTLRHNHVC 300

QY 301 VLKQEHFEMWDEQLFQTSRLILIGETIKIYIEDVYVGHLSGHNFLKRPDELLFNKQFOYQ 360
 Db 301 VLKQEHFEMWDEQLFQTSRLILIGETIKIYIEDVYVGHLSGHNFLKRPDELLFNKQFOYQ 360

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QY 361 NR|A|E|N|T|Y|H|H|P|D|P|F|Q|I|H|D|K|Y|N|Q|O|F|T|N|N|S|I|L|H|G|T|O|V|E|S|F|T|Q|I|A|G|V 420
Db 318 NR|I|S|E|N|T|Y|H|H|P|D|P|F|N|I|D|D|E|S|F|K|O|F|L|Y|N|N|S|I|L|H|G|T|O|V|E|S|F|T|Q|I|A|G|V 377
QY 421 A|G|G|N|V|P|A|V|K|O|S|Q|A|S|I|D|S|R|Q|K|Y|O|S|F|N|E|Y|R|F|M|K|P|E|S|F|E|L|T|G|E|K|E|A|E|L|A|L 480
Db 378 A|G|G|N|V|P|A|V|K|O|S|Q|A|S|I|D|S|R|Q|K|Y|O|S|F|N|E|Y|R|F|M|K|P|E|S|F|E|L|T|G|E|K|E|A|E|L|A|L 437
QY 481 Y|G|I|D|A|V|E|L|P|A|L|V|E|K|R|P|D|A|I|F|G|E|T|V|E|G|A|P|F|S|L|K|G|M|G|N|V|I|C|S|P|A|Y|K|P|S|T|F|G|E|V 540
Db 438 Y|S|I|D|V|E|L|P|A|L|V|E|K|R|P|D|A|I|F|G|E|T|V|E|G|A|P|F|S|L|K|G|M|G|N|V|I|C|S|P|A|Y|K|P|S|T|F|G|E|V 497
QY 541 G|F|O|I|N|T|A|S|I|O|S|I|C|N|N|V|K|G|C|P|F|T|S|F|V|P|D|P|E|L|I|K|T|V|T|N|A|S|S|R|S|G|L|D|I|N|P|T|V|L|K|R 600
Db 498 G|F|K|I|N|T|A|S|I|O|S|I|C|N|N|V|K|G|C|P|F|T|S|F|V|O|D|P|O|P|T|K|T|A|T|N|A|S|A|S|H|R|D|I|N|P|T|V|L|K|R 557
QY 601 S|T|E|L 604
Db 558 S|T|E|L 561

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RESULT 7

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Q9PW89 PRELIMINARY; PRT; 607 AA.
ID Q9PW89;
AC Q9PW89;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Prostaglandin endoperoxide synthase-2.
GN PGS-2.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCB|_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=20181763; PubMed=10715542;
RA Roberts S.B., Langenau D.M., Goetz F.W.;
RT "Cloning and characterization of prostaglandin endoperoxide synthase-1
RT and -2 from the brook trout update.";
RL Mol. Cell. Endocrinol. 160:89-97(2000).
DR EMBL; AF158373; AAD45896.1; -.
DR HSSP; 005769; ICVU.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR GO; GO:0006979; P:response to oxidative stress; IEA.
DR InterPro; IPR002007; Anim_peroxidase.
DR InterPro; IPR002016; Peroxidase.
DR Pfam; PF03098; An_peroxidase; 1.
DR PRINTS; PR00457; ANPEROXIDASE.
DR PROSITE; PS50292; PEROXIDASE_3; 1.
SQ SEQUENCE 607 AA; 69150 MW; 91CBF7BAEDD96B0 CRC64;

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Query Match 74.9%; Score 2425; DB 13; Length 607;
 Best Local Similarity 71.7%; Pred. No. 188;

Matches 431; Conservative 81; Mismatches 85; Indels 4; Gaps 3;

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QY 6 L|L|C|A|V|L|S|H|T|A|N|C|S|H|P|C|O|N|G|V|C|M|S|V|G|F|D|Y|K|C|C|T|T|G|F|G|E|N|C|S|T|P|E|L|T|K|L 65
Db 9 L|L|V|G|L|Y|F|C|G|V|D|P|C|A|Q|P|E|N|G|L|C|N|S|K|G|F|V|E|C|C|T|T|G|Y|G|K|N|C|T|P|E|L|T|W|I|K|I 68
QY 66 F|L|K|P|T|V|H|Y|L|T|H|F|K|G|F|N|V|N|N|I|P|L|R|N|A|I|S|Y|V|T|S|H|I|D|S|P|T|N|A|D|Y|G|K|S|W 125
Db 69 S|L|K|E|P|N|T|V|H|Y|L|T|H|G|L|M|W|I|N|K|I|T|F|R|A|I|S|Y|V|T|S|H|I|D|S|P|T|N|A|D|Y|G|K|S|W 128
QY 126 E|A|E|N|S|Y|T|R|A|L|P|V|D|D|C|T|P|L|G|V|G|K|Q|L|P|S|N|E|I|V|E|K|L|L|R|R|K|I|D|P|Q|G|S|N|M|F|A 185
Db 129 E|A|Y|N|S|Y|T|R|K|L|P|L|P|K|D|C|P|T|P|G|T|A|G|R|A|V|L|P|V|K|L|V|E|K|V|L|L|R|K|R|I|P|D|Q|S|N|M|F|A 188
QY 186 F|F|A|G|H|T|H|O|F|K|T|D|H|K|G|R|A|T|N|G|L|G|H|G|V|D|I|N|H|Y|G|T|L|R|A|Q|R|K|L|R|F|K|G|K|K|Y|Q|I|I|D 245

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Db 189 F|F|Q|H|T|H|O|F|K|S|D|L|K|G|R|A|T|N|G|H|G|V|D|I|N|H|Y|G|D|S|L|R|Q|H|K|L|R|F|K|G|K|K|Y|Q|I|N|G 248
QY 246 E|A|E|N|P|V|K|T|O|A|E|N|I|P|P|Q|V|E|H|L|R|A|V|G|Q|E|V|G|L|V|G|M|V|A|T|I|W|L|R|E|H|R|V|C|D|V|K|O|E 305
Db 249 E|A|V|P|L|V|R|E|V|G|A|E|N|H|P|Q|V|E|H|R|F|R|A|V|G|H|E|H|G|I|V|G|L|M|V|A|T|I|W|L|R|E|H|R|V|C|D|V|K|O|E 308
QY 306 H|P|E|G|E|Q|L|F|Q|R|L|L|I|G|T|I|K|I|V|I|E|D|Y|Q|H|L|S|G|H|F|K|L|K|P|E|L|F|N|K|O|Y|O|R|I|A 365
Db 309 H|P|E|W|D|E|R|L|F|Q|T|R|L|L|I|G|T|I|K|I|V|I|E|D|Y|Q|H|L|S|G|H|F|Q|L|K|P|E|L|F|N|K|O|Y|O|R|I|A 368
QY 366 E|F|N|T|Y|H|H|P|D|P|T|F|Q|I|H|D|K|Y|N|Q|O|F|T|N|N|S|I|L|H|G|T|O|V|E|S|F|T|Q|I|A|G|V|A|G|R|N 425
Db 369 E|F|N|T|Y|H|H|P|D|P|T|S|I|E|R|A|T|T|P|Q|F|N|N|S|L|V|E|H|G|T|N|L|V|E|S|F|T|Q|I|A|G|V|A|G|R|N 428
QY 426 V|P|P|A|V|K|S|Q|A|S|I|D|S|R|Q|K|Y|O|S|F|N|E|Y|R|F|M|K|P|E|S|F|E|L|T|G|E|K|E|A|E|L|A|L|G|D|I 485
Db 429 L|P|P|A|V|A|V|A|K|A|L|H|S|R|D|W|R|Q|S|L|N|A|Y|R|R|F|N|R|A|T|S|F|D|L|G|T|E|L|A|E|L|S|I|G|D|V 488
QY 486 A|V|E|L|P|A|L|V|E|K|R|P|D|A|I|F|G|E|T|V|E|G|A|P|F|S|L|K|G|M|G|N|V|I|C|S|P|A|Y|K|P|S|T|F|G|E|V|G|F|Q|I 545
Db 489 A|V|E|L|P|G|L|V|R|P|R|P|A|V|G|E|T|V|E|G|A|P|F|S|L|K|G|M|G|N|V|I|C|S|P|E|Y|W|P|S|T|F|G|S|V|G|F|D|Y 548
QY 546 N|T|A|S|I|O|S|I|C|N|N|V|K|G|C|P|F|T|S|F|V|D|P|E|L|I|K|T|V|T|N|A|S|S|R|S|G|L|D|I|N|P|T|V|L|K|R|S|T|E 603
Db 549 N|T|A|S|L|R|V|C|S|N|V|K|G|C|P|F|T|S|F|V|D|P|E|L|I|K|T|V|T|N|A|S|S|I|E|A|H|L|K|G|M|P|G|V|F|K|R|T|L|E 606
QY 604 L 604
Db 607 L 607

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RESULT 8

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Q9W715 PRELIMINARY; PRT; 607 AA.
ID Q9W715;
AC Q9W715;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cyclooxygenase-2 Precursor.
GN COX-2.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCB|_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Zou J., Neuman N., Holland J., Belosevic M., Cunningham C.,
RA Secomb C.J., Rowley A.F.;
RT "Fish macrophages express a cyclooxygenase-2 homologue following
RT activation.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ238307; CAB46017.1; -.
DR HSSP; 005769; ICVU.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR GO; GO:0006979; P:response to oxidative stress; IEA.
DR InterPro; IPR002007; Anim_peroxidase.
DR InterPro; IPR002016; Peroxidase.
DR Pfam; PF03098; An_peroxidase; 1.
DR PRINTS; PR00457; ANPEROXIDASE.
DR PROSITE; PS50292; PEROXIDASE_3; 1.
SQ SEQUENCE 607 AA; 69384 MW; 6EFP443C04CD3D9 CRC64;

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Query Match 74.7%; Score 2417; DB 13; Length 607;
 Best Local Similarity 71.2%; Pred. No. 8.ee-188;

Matches 428; Conservative 82; Mismatches 87; Indels 4; Gaps 3;

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QY 21 C|Y|C|L|O|O|X|Y|G|E|N|A|S|E|2|
Db 21 C|Y|C|L|O|O|X|Y|G|E|N|A|S|E|2|
QY 20 P|O|T|E|N|T|I|A|L|
Db 20 P|O|T|E|N|T|I|A|L|
QY 607 C|Y|C|L|O|O|X|Y|G|E|N|A|S|E|2|
Db 607 C|Y|C|L|O|O|X|Y|G|E|N|A|S|E|2|
QY 69384 M|W|; 6EFP443C04CD3D9 CRC64;
Db 69384 M|W|; 6EFP443C04CD3D9 CRC64;

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QY 6 LLLCAVLAISHTANPCSHPCONRGVCMVSGVFDQKCDCTRTGFGNGSTPELITRL 65
 Db 9 LLLAAGLVFCEGVDPCCAPCCENRGICNSKGFDPNDECCTRTGFGNGSTPELITRL 68
 QY 66 FLKRPNTVHYILTHFKGFNNVNNIPFLRNAMSIVLTSLRSHLIDSPPTVADYKYSW 125
 Db 69 SLKRPNTVHYILTHFKGIMVNNITVFRNAMSIVLTSLRSHLIDSPPTVADYKYSW 128
 QY 126 EAFSNLSYVTRALPVPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIIDPQSNMFA 185
 Db 129 EAVSNLFFYTRTLPLPLPKDCPTPMGTAGRAVLBDVNLVVEKLLRRKFIIDPQSNMFA 188
 QY 186 FPAQHFTHQFETKDHKGAFNGLGVDLNIHYETLARQRKLRFKDGKQKRLVLDG 245
 Db 189 FPAQHFTHQFETKDHKGAFNGLGVDLNIHYETLARQRKLRFKDGKQKRLVLDG 248
 QY 246 EYRPVAVKDTQAEMLTYPVPEHLRFVAVGQEVFGVGLMMYATITLREHNRVCDVLKOE 305
 Db 249 EYRPVAVKDTQAEMLTYPVPEHLRFVAVGQEVFGVGLMMYATITLREHNRVCDVLKOE 308
 QY 306 HPEWGEQOLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFQYQNR1A 365
 Db 309 HPEWGEQOLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFQYQNR1A 368
 QY 366 BENTLYHMHPLPDPFQIHDOKNYQOFTYNNSTLLEHGILQFVESFTROIAGRVAGRN 425
 Db 369 BENTLYHMHPLPDPFQIHDOKNYQOFTYNNSTLLEHGILQFVESFTROIAGRVAGRN 428
 QY 426 VPBAVQVQASIDOSRQMKYOSFNEYRKRFLKPYSEFEELTGKEMSAELBALYGDID 485
 Db 429 LEPALVGAAKLLEHNRDQYOSINAVRRRPMRYVTSFEDLTGETELAAELSLYGDVD 488
 QY 486 AVELYVALLIVEKRPDAIFGETWVEVGAPELSKGLMGVNTICSPAYKKESTFGGEVFOI 545
 Db 489 AVELYVALLIVEKRPDAIFGETWVEVGAPELSKGLMGVNTICSPAYKKESTFGGEVFOI 548
 QY 546 NTAISIOSLICNNVKG-CPEFTSEVPD-PELITKTITINASSRSGLDINPTVYLKKEST 603
 Db 549 NTAISIOSLICNNVKG-CPEFTSEVPD-PELITKTITINASSRSGLDINPTVYLKKEST 606
 QY 604 L 604
 Db 607 L 607

RESULT 9
 Q8UH43 PRELIMINARY; PRT; 601 AA.
 ID 08UH43
 AC 08UH43
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Prostaglandin G/H synthase 2.
 GN PTGS2.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCB1_TaxID=7955;
 RN NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12011329;
 RA Grosser T., Yustiff S., Cheskis E., Pack M.A., Fitzgerald G.A.;
 RT "Developmental expression of functional cyclooxygenases in
 RT zebrafish."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:8418-8423 (2002).
 EMBL: AY028585; AAK3031.1; -.
 DR GO: GO:0004601; F:peroxidase activity; IEA.
 DR GO: GO:0006979; P:response to oxidative stress; IEA.
 DR InterPro: IPR002007; Antim_peroxidase.
 DR InterPro: IPR006209; BGF like.
 DR InterPro: IPR002016; peroxidase.

DR Pfam: PF03098; An peroxidase; 1.
 DR Pfam: PF00008; BGF; 1.
 DR PRINTS: PR00457; ANPEROXIDASE.
 DR PROSITE: PS02922; PEROXIDASE_3; 1.
 SQ SEQUENCE 601 AA; 68672 MW; A8552C56521DD0C1 CRC64;
 Query Match 72.0%; Score 2331; DB 13; Length 601;
 Best Local Similarity 67.8%; Pred. No. 8,6e-181;
 Matches 410; Conservative 95; Mismatches 86; Indels 14; Gaps 3;
 QY 7 LLLCAVLAISHTANPCSHPCONRGVCMVSGVFDQKCDCTRTGFGNGSTPELITRL 60
 Db 4 LVCIVLSSIMIFPBGXVDPCCAPCCQGVCLSGADAYBCDCTRTGFGNGCTPELITRL 63
 QY 61 TRIKLFKPTNTVHYILTHFKGFNNVNNIPFLRNAMSIVLTSLRSHLIDSPPTVADY 120
 Db 64 TRIKALPRNVVHYILTHFKGIMVNNITVFRNAMSIVLTSLRSHLIDSPPTVADY 123
 QY 121 GYKSWAESNLSYVTRALPVPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIIDPQGS 180
 Db 124 GYKSWAESNLSYVTRALPVPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIIDPQGS 176
 QY 181 NMFAFPAQHFTHQFETKDHKGAFNGLGVDLNIHYETLARQRKLRFKDGKQKRLVLDG 240
 Db 177 SLMFAPFAQHFTHQFETKDHKGAFNGLGVDLNIHYETLARQRKLRFKDGKQKRLVLDG 236
 QY 241 QIIDEMVPTVAVKDTQAEMLTYPVPEHLRFVAVGQEVFGVGLMMYATITLREHNRVCD 300
 Db 237 QVVDGEVVPVAVKDTQAEMLTYPVPEHLRFVAVGQEVFGVGLMMYATITLREHNRVCD 296
 QY 301 VIKQHPHWEQOLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFQYQ 360
 Db 297 IKQHPHWEQOLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFQYQ 356
 QY 361 NTAISIOSLICNNVKG-CPEFTSEVPD-PELITKTITINASSRSGLDINPTVYLKKEST 420
 Db 357 NTAISIOSLICNNVKG-CPEFTSEVPD-PELITKTITINASSRSGLDINPTVYLKKEST 416
 QY 421 AGRVAVPQVQASIDOSRQMKYOSFNEYRKRFLKPYSEFEELTGKEMSAELBALYGDID 480
 Db 417 SGRVAVPQVQASIDOSRQMKYOSFNEYRKRFLKPYSEFEELTGKEMSAELBALYGDID 476
 QY 481 YGDIIDAVELYPALLIVEKRPDAIFGETWVEVGAPELSKGLMGVNTICSPAYKKESTFG 540
 Db 477 YGDIIDAVELYPALLIVEKRPDAIFGETWVEVGAPELSKGLMGVNTICSPAYKKESTFG 536
 QY 541 GQIINTASIOSLICNNVKG-CPEFTSEVPD-PELITKTITINASSRSGLDINPTVYLKKE 599
 Db 537 GQIINTASIOSLICNNVKG-CPEFTSEVPD-PELITKTITINASSRSGLDINPTVYLKKE 596
 QY 600 RSTEL 604
 Db 597 RSTEL 601

RESULT 10
 Q9TT26 PRELIMINARY; PRT; 449 AA.
 ID 09TT26
 AC 09TT26
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Cyclooxygenase-2 (Fragment).
 GN COX-2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OC NCB1_TaxID=9823;
 RN NCB1_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=breed yorkshire-landrace; TISSUE=Endometrium;
 RA Palin M.F., Guay F., Beaudry D., Laforest J.P., Matte J.J.;
 RT "Expression of cyclooxygenase-1 (COX-1) and cyclooxygenase-2 (COX-2)

RT in swine endometrial tissue."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF207824; AAF20942.1; -.
 DR HSP; Q05769; IDDX.
 DR GO: GO:0004601; F:peroxidase activity; IEA.
 DR GO: GO:0006979; P:response to oxidative stress; IEA.
 DR InterPro: IPR002007; Anim_peroxidase.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF03098; An_peroxidase; 1.
 DR PRINTS: PR00457; ANPEROXIDASE.
 DR PROSITE: PS50292; PEROXIDASE_3; 1.
 FT NON TER 1
 FT NON TER 449
 SQ SEQUENCE 449 AA; 52268 MW; 5910B7CC2A7CA17F CRC64;

Query Match 67.3%; Score 2198; DB 6; Length 449;
 Best Local Similarity 90.0%; Pred. No. 3.7e-170;
 Matches 404; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

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QY 88 VNNIPPLRNALMSYVITSSHLIDSPPTNADYGYKSWAFAFSLSYTRALPPVDDCPT 147
DB 1 VNNIPPLRNALMSYVITSSHLIDSPPTNADYGYKSWAFAFSLSYTRALPPVDDCPT 60
QY 148 PLGVKSKQLPDSNEIVEKLLLRKFTPPQSSNMMAFEAOFHTQFRTDHRKGPART 207
DB 61 PMGVKSKQLPDSNEIVEKLLLRKFTPPQSSNMMAFEAOFHTQFRTDHRKGPART 120
QY 208 NGLGHGVDLNIHGETTARQKRLRFKDGKMKYQIIDGEMYPPTVDTQAEMLTPQVPE 267
DB 121 KQCGHGVDSLHYGESLERQHKRLRFKDGKMKYQIIDGEMYPPTVDTQAEMLTPQVPE 180
QY 268 HIRFVAGQGVGLVRLMMYATITWLREHNRVCDVLKQEHPEWDEQLFQTSRLILIGETI 327
DB 181 HIRFVAGQGVGLVRLMMYATITWLREHNRVCDVLKQEHPEWDEQLFQTSRLILIGETI 240
QY 328 KIVIEDYVOHLGSGYHFKLFEPDELLFNKQFOYONRLAENFLYHMHPLLEPTQIHDOK 387
DB 241 KIVIEDYVOHLGSGYHFKLFEPDELLFNKQFOYONRLAENFLYHMHPLLEPTQIHDOK 300
QY 388 YNYQOFLYNNLSILHEGITOFESEFTROIAGRVAGGRNVPRAVKVQSASIDOSROMKYQ 447
DB 301 YNYQOFLYNNLSILHEGITOFESEFTROIAGRVAGGRNVPRAVKVQSASIDOSROMKYQ 360
QY 448 SNEERKRFMLKPYSPFELTGEKMSALELALYGDIDAVELYPALLVEKPPDAIFGFT 507
DB 361 SNEERKRFMLKPYSPFELTGEKMSALELALYGDIDAVELYPALLVEKPPDAIFGFT 420
QY 508 MVEVGAPEFLKGLMGNVICSPAYWKSTF 536
DB 421 MVEVGAPEFLKGLMGNVICSPAYWKSTF 449

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RESULT 11
 Q7TFB3 PRELIMINARY; PRT; 604 AA.
 AC Q7TFB3;
 DT 01-OCT-2003 (TIREMBLrel. 25, Created)
 DT 01-OCT-2003 (TIREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TIREMBLrel. 25, Last annotation update)
 DE Rh10.
 OS Rhesus cytomegalovirus (strain 68-1) (RHCMV).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 CX NCBI_TaxID=103930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=68-1;
 RX PubMed=12767982;
 RA Hansen S.G., Strelow L.I., Franchi D.C., Anders D.G., Wong S.W.;
 RT "Complete Sequence and Genomic Analysis of Rhesus Cytomegalovirus."
 RL J. Virol. 77:6620-6636(2003).
 DR EMBL: AY186194; AAP50751.1; -.
 SQ SEQUENCE 604 AA; 68380 MW; 6699F6ED8F7D44D5 CRC64;

Query Match 64.0%; Score 2071.5; DB 12; Length 604;
 Best Local Similarity 63.4%; Pred. No. 1.1e-159;
 Matches 330; Conservative 73; Mismatches 119; Indels 33; Gaps 6;

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QY 6 LILCAVIALSHTNPPCCSHPCQNRGCMVSGFYQYQCDCTRGTGYBNCSTPEFLTRIKL 65
DB 7 VLVYSLSHSRQPLPLPSVSKRGICMYGFHHYKDCDCHTFIDHDCCT---TRIKL 62
QY 66 FLKPTNTYHYIITHKGFNNVNNIPLRLNATMSYVLTSRSHLIDSPPTNADYGYKSW 125
DB 63 FLKPDPTVYTYLTHFSTITWLVNINIPFLRAHMYRLTSRSLIDSPPTNADYGYKSW 122
QY 126 EAFSNLSYTRALPPVDDCPTPLGK-GRKQLPDSNEIVEKLLLRKFTPPQSSNMMAF 184
DB 123 EAFSNLSYTRALPPVDDCPTPLGKGRKQLPDAHAYVEKLLLRKFTPPQSSNMMAF 182
QY 185 AFEAOFHTQFRTDHRKGPARTNGLGVDLNIHGETTARQKRLRFKDGKMKYQIID 244
DB 183 AFEAOFHTQFRTDHRKGPARTNGLGVDLNIHGETTARQKRLRFKDGKMKYQIID 242
QY 245 GEMYPPTVDTQAEMLTPQVPEHLRFVAGQGVGLVRLMMYATITWLREHNRVCDVLKQ 304
DB 243 GEMYPPTVDTQAEMLTPQVPEHLRFVAGQGVGLVRLMMYATITWLREHNRVCDVLKQ 302
QY 305 EHPWGDDEQLFQTSRLILIGETIKIVIEDYVOHLGSGYHFKLFEPDELLFNKQFOYONRLA 364
DB 303 EHPWGDDEQLFQTSRLILIGETIKIVIEDYVOHLGSGYHFKLFEPDELLFNKQFOYONRLA 362
QY 365 AEFNTLYHMHPLLPDTPQIHDQKNVYQOFLYNNLSILHEGITOFESEFTROIAGRVAGGR 424
DB 363 SEFNLMYHSHSLMPAPFELDKTDYINLVNNSILMTHGITQLYESFTKQTAGRVAPL 422
QY 425 NVPRVQKVQSASIDOSROMKYQSPNEYKRFMLKPYE-SPELITGEKMSALELALYGD 483
DB 423 NVPRVQKVQSASIDOSROMKYQSPNEYKRFMLKPYE-SPELITGEKMSALELALYGD 469
QY 484 IDAVELYPALLVEKPPDAIFGFTMVEVGAPEFLKGLMGNVICSPAYWKSTFPGGEVGFQ 543
DB 470 IDAVELYPALLVEKPPDAIFGFTMVEVGAPEFLKGLMGNVICSPAYWKSTFPGGEVGFQ 529
QY 544 IINTASIOSLTCNNYKGPFTSFVSVDPELLK-----TYTNASSRSRGUD 589
DB 530 IINTASIOSLTCNNYKGPFTSFVSVDPELLK-----TYTNASSRSRGUD 589
QY 590 DINPVLAKENSTEL 604
DB 590 DINPVLAKENSTEL 604

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RESULT 12
 Q9N288 PRELIMINARY; PRT; 422 AA.
 AC Q9N288;
 DT 01-OCT-2000 (TIREMBLrel. 15, Created)
 DT 01-OCT-2000 (TIREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TIREMBLrel. 25, Last annotation update)
 DE Cyclooxygenase-2 (Fragment).
 GN COX-2.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Thoroughbred; TISSUE=Arterial endothelium;
 RA Ishida N., Sato F., Hasegawa T.;
 RT "Molecular cloning of equine COX-2 mRNA for cyclooxygenase-2."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB041771; BA049762.1; -.
 DR HSP; Q05769; IDDX.
 DR GO: GO:0004601; F:peroxidase activity; IEA.
 DR GO: GO:0006979; P:response to oxidative stress; IEA.

DR InterPro; IPR002007; Anim_peroxidase.
 DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PF03098; An_peroxidase; 1.
 DR PRINTS; PR00457; ANPEROXIDASE.
 DR PROSITE; PS50292; PEROXIDASE_3; 1.
 FT NON TER 1 422 1
 SQ SEQUENCE 422 AA; 48675 MW; 8F9792D936BC7B63 CRC64;
 Query Match 63.2%; Score 2047; DB 6; Length 422;
 Best Local Similarity 89.6%; Pred. No. 6.5e-158;
 Matches 378; Conservative 25; Mismatches 19; Indels 0; Gaps 0;

QY 131 LSYTRALPPVDDCPPLGVGKQQLPPSNIVKLLRRKFTDPQSSNMFAFPAFH 190
 DB 1 LSYTRALPPVADGCPMPGVKKEKLPDSKEIVKFLRRKFIPDPQSTNMFAFPAH 60
 QY 191 PTHQFETDKKRPATNGLGHVDLNIHYGETLARQRLRFKQKMYQIIDGEMYP 250
 DB 61 PTHQFETDKKRPATNGLGHVDLNIHYGETLARQRLRFKQKMYQIIDGEMYP 120
 QY 251 TVKDTQAEIYTPQVEEHLRFVAGQVEFGLVPGMMYATITWREHNRVCDVTKQHPK 310
 DB 121 TVKDTQAEIYTPQVEEHLRFVAGQVEFGLVPGMMYATITWREHNRVCDVTKQHPK 180
 QY 311 DQQLPQTSLLIGETIKIVIDYVQHLSGYHFKLKEDELLFNKQFOYONRIAEFNTL 370
 DB 181 DQQLPQTSLLIGETIKIVIDYVQHLSGYHFKLKEDELLFNKQFOYONRIAEFNTL 240
 QY 371 YHMHPLPPTFOIHQDKVYVQFIYNNSTLLEHGITQVESFTQAGRVAGGRVPPAV 430
 DB 241 YHMHPLPPTFOIHQDKVYVQFIYNNSTLLEHGITQVESFTQAGRVAGGRVPPAV 300
 QY 431 QKVSQASIDQSRMKTQSFNRYKRFMLKPYESFEELTGKEMSALEALYGDIDVELY 490
 DB 301 QKIASISQSEEMKQSLNRYKRFMLKPYESFEELTGKEMSALEALYGDIDVELY 360
 QY 491 PALVKKPRPDALFGFTWVEVGFSLKGLMGVVICSPAYWKSTGEGEVOIINTASI 550
 DB 361 PALVKKPRPDALFGFTWVEVGFSLKGLMGVVICSPAYWKSTGEGEVOIINTASI 420
 QY 551 QS 552
 DB 421 QS 422

RESULT 13
 097554 PRELIMINARY; PRT; 606 AA.
 AC 097554;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DB Cyclooxygenase-1.
 GN COX-1.
 OS Oryzctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCB1_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand White;
 RA Guan Y., Zhang Y., Breyer R.M., Davis L., Redha R., Chang S.,
 Breyer M.D.;
 RT "Intrarenal localization of cyclooxygenase-1 and -2 and their
 RT differential expression in acute hydropnephrotic kidney";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF026008; AAD01796.1; -
 DR HSSP; P05979; 1COE
 DR GO; GO:0004601; P:peroxidase activity; IEA.
 DR GO; GO:0006979; P:response to oxidative stress; IEA.
 DR InterPro; IPR002007; Anim_peroxidase.
 DR InterPro; IPR006210; IEGF.

DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PF03098; An_peroxidase; 1.
 DR PRINTS; PR00457; ANPEROXIDASE.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS50292; PEROXIDASE_3; 1.
 SQ SEQUENCE 606 AA; 69075 MW; DB751FD1E2F1CD77 CRC64;
 Query Match 63.2%; Score 2045.5; DB 6; Length 606;
 Best Local Similarity 85.1%; Pred. No. 1.5e-157;
 Matches 370; Conservative 85; Mismatches 112; Indels 19; Gaps 4;

QY 19 NPCCSHPCQNGVCMSVSPDYKDCDCTRTGYGNCSTPELITRIKLKLPPTNVHIL 78
 DB 40 NPCCYPCQHGQCVRVALLDRYQDCDCTRTGYSGNCTVDDLTWTRSSIRPSFTVHIL 99
 QY 79 THKGFNVNVPNIPPLNAINSVYLSHSLIDSPPTNADVGYSWEAFNSLYTTRAL 138
 DB 100 THKGFNVNVPNIPPLNAINSVYLSHSLIDSPPTNADVGYSWEAFNSLYTTRAL 158
 QY 139 PVPDDCPTPLGVKQKQQLPDSNEIVEKLLRRKEIPDPQSSNMFAFPAFHQFET 198
 DB 159 PVPDDCPTPLGVKQKQQLPDSNEIVEKLLRRKEIPDPQSSNMFAFPAFHQFET 218
 QY 199 DHRGPATNGLGHVDLNIHYGETLARQRLRFKQKMYQIIDGEMYPVADQAE 258
 DB 219 DHRGPATNGLGHVDLNIHYGETLARQRLRFKQKMYQIIDGEMYPVADQAE 278
 QY 259 MLYPQVPEHRLRFVAGQVEFGLVPGMMYATITWREHNRVCDVTKQHPKDEQLFQTS 318
 DB 279 MLYPQVPEHRLRFVAGQVEFGLVPGMMYATITWREHNRVCDVTKQHPKDEQLFQTS 338
 QY 319 RLILIGETIKIVIDYVQHLSGYHFKLKEDELLFNKQFOYONRIAEFNTLYHMHPLP 378
 DB 339 RLILIGETIKIVIDYVQHLSGYHFKLKEDELLFNKQFOYONRIAEFNTLYHMHPLP 398
 QY 379 DFPQHDQKYNVQOFLYNNSTLLEHGITQVESFTQAGRVAGGRVPPAVQXQSAI 438
 DB 399 DFPQHDQKYNVQOFLYNNSTLLEHGITQVESFTQAGRVAGGRVPPAVQXQSAI 458
 QY 439 DQSRQKVSFNFYRKRFLKPYESFEELTGKEMSALEALYGDIDAVELYPALLVERK 498
 DB 459 DQSRQKVSFNFYRKRFLKPYESFEELTGKEMSALEALYGDIDAVELYPALLVERK 518
 QY 499 RPDALFGFTWVEVGFSLKGLMGVVICSPAYWKSTGEGEVOIINTASIOSLICNNV 558
 DB 519 RPDALFGFTWVEVGFSLKGLMGVVICSPAYWKSTGEGEVOIINTASIOSLICNNV 578
 QY 559 KCCPFTSEVPDELIKIVTINASSRSGLDIDNPTVLKERTEL 604
 DB 579 KCCPFTSEVPDELIKIVTINASSRSGLDIDNPTVLKERTEL 606

RESULT 14
 080VQ3 PRELIMINARY; PRT; 593 AA.
 AC 080VQ3;
 DT 01-MAR-2002 (TEMBLrel. 20, Created)
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DB Cyclooxygenase.
 GN Squalus acanthias (Spiny dogfish).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Squalidae; Squalus.
 OC NCB1_TaxID=7797;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Rectal gland;
 RA Yang T., Forrest S., Stine N., Endo Y., Pasumaththy A., Aller S.,
 Forrest J.N. Jr., Scherman J.B., Briggs J.P.;
 RT "Cloning of a cyclooxygenase cDNA from dogfish shark, Squalus
 RT acanthias, and its role in the regulation of rectal gland chloride
 RT secretion";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF420317; AAL37727.1; -
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 DR GO; GO:0006979; P:response to oxidative stress; IEA.
 DR InterPro; IPR002007; Anim_peroxidase.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PF03098; An_peroxidase; 1.
 DR Pfam; PF00008; EGF; 1.
 DR PRINTS; PR00457; ANPEROXIDASE.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS50292; PEROXIDASE_3; 1.
 DR SEQUENCE 593 AA; 68274 MW; 85F2C870B04ED0F CRC64;

Query Match 63.1%; Score 2041.5; DB 13; Length 593;
 Best Local Similarity 62.1%; Pred. No. 3e-157;
 Matches 355; Conservative 101; Mismatches 111; Indels 5; Gaps 2;

QY 3 ARAAL-----LCANLASHTA-NPCSHPCQNRGVMSVGFDOYKDCCTRTGYGNCSTP 57
 Db 4 ARIILLPLCPKKAADTTAINPCYYPQNKGCICNVGKEGECDCCTRTGYGVNCTPP 63
 QY 58 EELTRIKLPLKPTENTVHYILTFKGFMMVNNIPLRANMSYVLTSSHLIDSPPTN 117
 Db 64 FMSRVHFKLSPSSMHVILHYKMLWIIINISFSDTLMKLVLTVANILPSPPTN 123
 QY 118 ADYGYKSWAFNSLYTRALPVPDCEPTPLGVKKQKLPDSNEIVEKLLRRKIPDP 177
 Db 124 SYTYVSWGYSNISITLRLPVPKDCPTPTGQYKKLPDSEQLAEFLRRKIPDP 183
 QY 178 QGSNMWFAFFAOFHFOFKTDHKGPAFTNGLGHVLDLNIYGETLAFQKRLRPFQKQ 237
 Db 184 QGSNMFAPFAOHFTHQFRTLDKGPFTKALGQVLDLTHYGDSLERQHLRLFKQK 243
 QY 238 MKYQIIDGMYRPTVKDTQAEMLYRPVVEHLRFVAGQEVFGVPLGMVYATITMLREHR 297
 Db 244 LKYQVNVGVPSPYSKXEARIQMKYPTSLDEBKRLAIGHDTFGLITGLMAYATITMLREHR 303
 QY 298 VCDVUKQEHREMGDEQLFQTSRLILGETIKIVIEDYVQHLSGYHFKLPDELLFNKQF 357
 Db 304 VCDILKEHPVMSDQLFQTRLILIGETIKIVIEDYVQHLSGYHFRMMFNELLFTHEF 363
 QY 358 QYONRIAAEFNTLYMHPLPPTFQIHQKXVQOFYNNNSILLEGITQFVSESTRQIA 417
 Db 364 QYSRIAYBFHDLHYMHPLMPDSTLVKQDSEYKQFLNNTDILLMGADALVESFSKOIA 423
 QY 418 GRVAGRVNPAVQKVSQASIDOSROMKXQSFNEYRKRPFMLKPYSEFELTGEKMSAEI 477
 Db 424 GRIGGRNIIHQSLHIAIATIEHGLLRFQRYNEIRKLLGLTPYKSFQELTGEREVARL 483
 QY 478 EALYGDIAVELYPALLYEKRPDAIFGETWVEGAPFSLKGLMGNVICSPAYWKPSTFG 537
 Db 484 EKLXGHIDAMEFYRALLLEAPNKNISIFGESWEMGAPFSLKGLMGNPICSPDYWKPSTFG 543
 QY 538 GEVGFQINTASIOSLICNNVKGCFSTFSVP 569
 Db 544 GKTGFQIVNTATPEKILCLNVKCPYGVGFHP 575

RESULT 15
 ID 08JH44 PRELIMINARY; PRT; 597 AA.
 AC 08JH44.
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Prostaglandin G/H synthase 1.
 GN PTGS1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_Taxid=7955;

RN [1]
 SEQUENCE FROM N.A.
 RP PubMed=12011329;
 RA Grosser T., Yusuf S., Cheskis E., Pack M.A., Fitzgerald G.A.;
 RT "Developmental expression of functional cyclooxygenases in
 zebrafish."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:8418-8423(2002).
 DR EMBL; AY028584; AAK31030.1; -
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 DR GO; GO:0006979; P:response to oxidative stress; IEA.
 DR InterPro; IPR002007; Anim_peroxidase.
 DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PF03098; An_peroxidase; 1.
 DR PRINTS; PR00457; ANPEROXIDASE.
 DR PROSITE; PS50292; PEROXIDASE_3; 1.
 DR SEQUENCE 597 AA; 68963 MW; A13593679926F292 CRC64;

Query Match 63.0%; Score 2040.5; DB 13; Length 597;
 Best Local Similarity 64.7%; Pred. No. 3.6e-157;
 Matches 359; Conservative 86; Mismatches 109; Indels 1; Gaps 1;

QY 15 SHTANPCSHPCQNRGVMSVGFDOYKDCCTRTGYGNCSTPEELTRIKLFLKPTNTY 74
 Db 30 SNTANPCCYPPQONOGICVRYGLERYECDCCTRTGYGNCCTIPELMTRYVRLKPSPNV 89
 QY 75 HYILTFKGFMMVNNIPLRANMSYVLTSSHLIDSPPTNADYGYKSWAFNSLY 134
 Db 90 HYILTFHFWMLNLR-SFLRDMLRKVLTVANILPSPPTNSRDYLNWVAYSNITY 148
 QY 135 TRALPVPDCEPTPLGVKKQKLPDSNEIVEKLLRRKIPPOGSNMWFAFFAOFHTQ 194
 Db 149 TRILPVPDCEPTPTMGTKIKLPDKLVEKMLRRNFRDQGTNLMFAFFAOFHTQ 208
 QY 195 PEKTHKGPATNGLGQVLDLNIYGETLAFQKRLRPFQKMKYQIIDGMYRPTVKD 254
 Db 209 FEKTHNRVGLGFTKLGQVAGHYGDSLRLQBLRLHKQKLYQVNLGDIYPTVLH 268
 QY 255 TQAEMLYRPVVEHLRFVAGQEVFGVPLGMVYATITMLREHRVCDVUKQEHREMGDEQL 314
 Db 269 AQVKMSYSPSVEEQDLAIGQEVFGLPLGLGMVYATITMLREHRVCEIILKQEHPTMGDEQL 328
 QY 315 FQTSRLILGETIKIVIEDYVQHLSGYHFKLPDELLFNKQFQYONRIAAEFNTLYMH 374
 Db 329 FQARLIIIGETIRIVIEYVQHLSGYHFKLPDITLFPNQFOYQNRISVEFNQIYMH 388
 QY 375 PLPPTFQIHQKXVQOFYNNNSILLEGITQFVSESTRQIAGRVAGRVNPAVQKVS 434
 Db 389 PLMPDSFYIDDHIOYSKFIPTNTSILTHYGLEKIVEAFSIQPAQIGGCHNHPVSGVA 448
 QY 435 QASIDOSROMKXQSFNEYRKRPFMLKPYSEFELTGEKMSAELEALYGDIAVELYPALI 494
 Db 449 ERVIVSEHLLQFPNEYRKRPFMLKPYTSFELTGEQMSAELEALYGHIDAMEFYPALI 508
 QY 495 VEKRPDAIFGETWVEGAPFSLKGLMGNVICSPAYWKPSTFGGEVGFQINTASIOSLI 554
 Db 509 LEKTRPGAIVGESWEMGAPFSLKGLMGNPICSPDYWKPSTFGKRTGDIYNSATLKLV 568
 QY 555 CNNVKGCFSTFSVP 569
 Db 569 CLNTKWCPEYVSFHTP 583

Search completed: April 24, 2004, 07:21:03
 Job time : 75 secs

Blank

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 07:22:17 ; Search time 12760 Seconds

(without alignments)
11504.926 Million cell updates/sec

Title: US-08-064-271-11

Sequence: 1 GTCGAGAACTCTCTCAGCAG.....GATTAAGAAAAAAAAAG 3387

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_ba:*
- 2: gb_hg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_da:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_scs:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_hg_hum:*
- 31: em_hg_inv:*
- 32: em_hg_other:*
- 33: em_hg_mus:*
- 34: em_hg_pln:*
- 35: em_hg_rtd:*
- 36: em_hg_mam:*
- 37: em_hg_vrt:*
- 38: em_sy:*
- 39: em_hgo_hum:*
- 40: em_hgo_mus:*
- 41: em_hgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3387	100.0	3387	6	124360
2	3385.4	100.0	3387	6	AX328834
3	3379	99.8	3387	6	AR380505
4	3379	99.8	3387	6	AX082878
5	3379	99.8	3387	6	HIMCYCLOX
6	3375.8	99.6	3387	6	AR029278
7	3374.2	99.6	3387	6	AR106720
8	3374.2	99.6	3387	6	AR202531
9	3215	94.9	3394	9	BC013734
10	3161.4	93.3	3362	9	HUMENDOSYN
11	3087	91.1	3669	9	AY151286
12	1912.2	56.5	3314	4	U97696
13	1810.2	53.4	1815	9	AY462100
14	1803.2	53.2	1834	6	AR055229
15	1803.2	53.2	1834	6	AR055235
16	1727.8	51.0	10997	9	HUMPTGS2
17	1727	51.0	9453	6	AX332842
18	1727	51.0	9453	6	HSU04636
19	1720.6	50.8	11449	9	AY229989
20	1720.6	50.8	12551	9	AY382629
21	1719	50.8	84412	9	HS973M2
22	1650.8	48.7	3398	4	AF027334
23	1650.4	48.7	3621	4	AY028563
24	1621.6	47.9	3509	6	AR411929
25	1621.6	47.9	3509	6	AR411930
26	1620	47.8	3632	6	AX082874
27	1605.2	47.4	3489	4	AF031698
28	1605	47.4	3498	4	AY044905
29	1583	46.7	3483	4	CAU68486
30	1552.2	45.8	2763	10	CPCOX2
31	1528.6	45.1	4152	6	AX306255
32	1528.6	45.1	4152	10	MUSGRIPIGHS
33	1525.8	45.0	3986	6	AR029276
34	1525.8	45.0	3986	10	MUSPCSF
35	1476.6	43.6	1812	6	AR411931
36	1476.6	43.6	1812	6	AR411932
37	1446	42.7	2340	10	MUSPEHSB
38	1432.8	42.3	1984	10	AY065644
39	1431.8	42.3	4154	10	S67722
40	1431.8	42.3	4404	10	AF233596
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DEFINITION Sequence 11 from patent US 5543297.
ACCESSION 124360
VERSION 124360.1 GI:1604230
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3387)
AUTHORS Cromlish, W.A., Kennedy, B.P., O'Neill, G., Vickers, P.J., Wong, E. and Mancini, U.A.
TITLE Human cyclooxygenase-2 cDNA and assays for evaluating cyclooxygenase-2 activity

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: US 5543297-A 11 06-AUG-1996;
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 AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
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 JOURNAL Patent: US 6607879-A 1050 19-AUG-2003;

FEATURES
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LOCUS      AX082878
DEFINITION      Sequence 7 from Patent WO0111026.
ACCESSION      AX082878
VERSION      AX082878.1 GI:13184807
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE      1
AUTHORS      Gierse, J.K.
TITLE      Canine cyclooxygenase-1 (cox-1) and cyclooxygenase-2 (cox-2)
JOURNAL      Patent: WO 0111026-A 7 15-FEB-2001;
G.D. SEARLE & CO. (US)
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 ACCESSION M90100.1 GI:161253
 VERSION cyclooxygenase-2; prostaglandin synthase.
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 SOURCE ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 AUTHORS Hla,T. and Neilson,K.
 TITLE Human cyclooxygenase-2 cDNA
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (16), 7384-7388 (1992)
 MEDLINE 9236465

PUBMED 1380156
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 Best Local Similarity 99.8%; Pred.No. 0;
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 LOCUS Sequence 19 from patent US 6107087.
 DEFINITION
 ACCESSION ARI06720
 VERSION ARI06720.1 GI:12821250
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 3387)
 O'Neill, G.P. and Mancini, J.A.
 TITLE High level expression of human cyclooxygenase-2
 JOURNAL Patent: US 6107087-A 19 22-AUG-2000;
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ACCESSION AR202531
VERSION AR202531.1 GI:20257070
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3387)
AUTHORS O'Neill, G.P. and Mancini, J.A.
TITLE High level expression of human cyclooxygenase-2
JOURNAL Patent: US 6362327-A 19 26-MAR-2002;
FEATURES
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QY	2281	GCATCTTCATGATGATCATTAGAAGTAACTGTTGAAATTTTAAATGTTAACTGTTGGGTA		2340
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LOCUS			
DEFINITION	BC013734	3394 bp mRNA linear PRI 04-OCT-2003	
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	G/H synthase and cyclooxygenase), mRNA (cDNA clone MGC:9576		
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ACCESSION	BC013734		
VERSION	BC013734.1	GI:15489264	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,		
	Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,		
	Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,		
	Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hecht,F.,		
	Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.W., Hong,L.,		
	Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.U.,		
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	Carninci,P., Brange,C., Raha,S.S., Loquellano,N.A., Peters,G.U.,		
	Abrahamson,R.D., Mullany,S.J., Bossek,S.A., McEwan,P.J.,		
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	Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,		
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	Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,R., Myers,R.M.,		
	Butterfield,Y.S., Krzywinska,M.I., Skalska,U., Smalhus,D.E.,		
	Scherer,A., Schein,J.E., Jones,J. and Morris,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length		
JOURNAL	human and mouse cDNA sequences		
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
REFERENCE	22388257		
AUTHORS	Strausberg,R.		
TITLE	2 (bases 1 to 3394)		
JOURNAL	Direct Submission		
COMMENT	Submitted (04-SEP-2001) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
	NIH-MGC Project URL: http://mgc.nci.nih.gov		
	Contact: MGC help desk		
	Email: cgabbs-r@mail.nih.gov		
	Tissue Procurement: DCTD/DTP/dazdar		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA library Arrayed by: The I.M.A.-G.E. Consortium (LIML)		
	DNA Sequencing by: Baylor College of Medicine Human Genome		
	Sequencing Center		
	Center code: BCM-HGSC		
	Web site: http://www.hgsc.bcm.tmc.edu/cdna/		
	Contact: amgc@bcm.tmc.edu		
	Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loutsseg, H.,		
	Kowitz, C.R., Shedd, A.J., Martin, R.G., Muzny, D.M., Nanavati,		
	A.N., Gibbs, R.A.		

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/ILN at: <http://image.llnl.gov>
 Series: IRAP Plate: 21 Row: n Column: 20
 This clone was selected for full length sequencing because it
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ACCESSION U15326
VERSION U15326.1 GI:291987
KEYWORDS endoperoxide synthase type II.
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REFERENCE 1 (bases 1 to 3362)
AUTHORS Jones,D.A., Carlton,D.P., McIntyre,T.M., Zimmerman,G.A. and
Prescott,S.M.
JOURNAL Molecular cloning of human prostaglandin endoperoxide synthase type
MEDLINE II and demonstration of expression in response to cytokines
PUBMED J. Biol. Chem. 268 (12), 9049-9054 (1993)
COMMENT 8473346
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 ACCESSION AY151286
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3669)
 AUTHORS Duan, Y.

TITLE Direct Submission
 JOURNAL Submitted (18-SEP-2002) Department of Pathophysiology, Key
 Laboratory of Pulmonary Disease of Ministry of Health, Tongji
 Medical College, Huazhong University of Science and Technology,
 Hangkong Road 13, Wuhan, Hubei 430030, China
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RESULT 12
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 LOCUS Oryctolagus cuniculus cyclooxygenase-2 (COX-2) mRNA, complete cds.
 DEFINITION
 ACCESSION U97696
 VERSION U97696.1 GI:2109296
 KEYWORDS
 SOURCE Oryctolagus cuniculus (rabbit)
 ORGANISM Oryctolagus cuniculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE 1 (bases 1 to 3314)
 Guan, Y., Chang, M., Cho, W., Zhang, Y., Redha, R., Davis, L., Chang, S.,

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TITLE
Dubois, R.N., Hao, C.M. and Breyer, M.
Cloning, expression, and regulation of rabbit cyclooxygenase-2 in
renal medullary interstitial cells
JOURNAL
Am. J. Physiol. 273 (1 Pt 2), F18-F26 (1997)
MEDLINE
97393071
PUBMED
9249588
AUTHORS
2 (bases 1 to 3314)
Guan, Y., Chang, M., Cho, W., Zhang, Y., Redha, R., Davis, L., Chang, S.,
Dubois, R.N., Hao, C.-M. and Breyer, M.D.
TITLE
Direct Submission
JOURNAL
Submitted (15-APR-1997) Nephrology, Vanderbilt University Medical
Center, Nashville, TN 37232-2372, USA
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Location/Qualifiers
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ORIGIN

Query Match 56.5%; Score 1912.2; DB 4; Length 3314;
 Best Local Similarity 78.6%; Pred. No. 0;
 Matches 2632; Conservative 0; Mismatches 618; Indels 99; Gaps 25;

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Qy      179 AACCGAGTGATATGATGATGTGGATTTGACGATTAATGCGATGTACCGGAGCA 238
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Qy      239 GGAATCTATGAGAAATGCTCAACACCGGAAATTTTGAAGAATTAATATTCTG 298
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DEFINITION AY462100
ACCESSION AY462100.1 GI:38565064
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1815)
AUTHORS Sharma,S.V. and Aronstam,R.S.
TITLE Isolation of cDNA coding for cyclooxygenase 2 (COX2)
JOURNAL Unpublished
2 (bases 1 to 1815)
AUTHORS Sharma,S.V. and Aronstam,R.S.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-2003) Guthrie cDNA Resource Center, Guthrie
Research Institute, 1 Guthrie Square, Sayre, PA 16840, USA
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ORIGIN
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Matches 1812; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 61 TCGTGTCCCAACCCATGCTCAAAACCGAGGTGATGATGATGATGATGATGATGATGAT 120
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QY 398 TATGTTGATCATTCAGATCAATTTGATTTGACAGTCCACCACTTACATGCTGACAT 457
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QY	878	TACCTCTCAAGTCTCCAGCATCTACGGTTTGCTGTGGGAGAGAGGCTCTTGCTG	937
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QY	938	GTCCTGTGCTGATGATGTAATGCCCAATCTGGCTGGGAAAACAACAAGATATGTAT	997
Db	841	GTCCTGTGCTGATGATGTAATGCCCAATCTGGCTGGGAAAACAACAAGATATGTAT	900
QY	998	GTCCTTAAACAGAGCATCTCGAATGGGGTGAATGAGCAATGTTCCAGACAAGCGGCTA	105
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QY	1358	GCTGCTGGTAAGGAATGTTCCACCGGCAATACAGAAAGTATCAAGGCTTCATTGACAG	1417
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SOURCE	Unknown.		
ORGANISM	Unclassified.		
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AUTHORS	Young,D.A., O'Banion,M.K. and Winn,V.D.		
TITLE	Screening assays for inhibitors of mammalian prostaglandin H synthase-2		
JOURNAL	Patent: US 5837479-A 3 17-NOV-1998;		
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 1 (bases 1 to 1834)
 AUTHORS Young, D.A., O'Banion, M.K. and Winn, V.D.
 TITLE Screening assays for inhibitors of mammalian prostaglandin H synthase-2
 JOURNAL Patent: US 5837479-A 14 17-NOV-1998;
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 Best Local Similarity 99.0%; Pred. No. 0;
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GenCore version 5.1.6
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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	3379.9	99.8	3387	6	AAf21115 Human low
5	3379.9	99.8	3387	6	AB294344 Human cyc
6	3379.9	99.8	3387	7	AB296809 Human cyc
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18	2513.4	74.2	2563	7	AB296811 Human cyc
19	1819.2	53.7	1834	5	AAf59635 Human pro
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21	1787.2	52.8	1834	5	AAf59635 Human pro
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25	1727	51.0	9453	6	AB296810 Human cyc
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ALIGNMENTS

RESULT 1	AA089376	standard; cDNA; 3387 BP.
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AC	AA089376	
XX	AA089376	
DT	25-MAR-2003	(revised)
DT	28-SEP-1995	(first entry)
XX	Human cyclooxygenase-2 CDNA.	
XX	Cyclooxygenase-2; COX-2; COX-1; inhibitor; screening; osteosarcoma; ss.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
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XX	W09509238-A1.	
XX	06-APR-1995.	
XX	13-SEP-1994;	94MO-CA000501.
XX	27-SEP-1993;	93US-00084033.
XX	(MERI) MERCK FROST CANADA INC.	
XX	Oneil GP, Mancini JA;	
XX	WPI, 1995-147436/19.	
XX	P-PSDB; AAR72228.	
XX	High level expression of human cyclooxygenase (COX)-2 - using new 3' flanking region from COX-1, useful in assays for identifying potent, selective or preferential inhibitors of COX-2.	
XX	Disclosure; Fig 2; 59pp; English.	
XX	Full-length cDNA derived from human osteosarcoma cells (given in	
XX	AA089376) encoded human COX-2 (AAR72228). High-level expression of COX-2	
XX	in COS7 cells was achieved using a vaccinia or baculovirus vector and a	
XX	construct in which COX-2 cDNA was attached at its 5' end to a 3' flanking	
XX	sequence of human COX-1 cDNA (AA089377). (Updated on 25-MAR-2003 to	
XX	correct PN field.)	

XX Sequence 3387 BP; 1010 A; 714 C; 632 G; 1031 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 3385.4; DB 2; Length 3387;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 901 TCTACGTTTGTGTGGGAGAGAGCTTTGCTGTGGTCTGTGATGATGATGC 960
DB 901 TCTACGTTTGTGTGGGAGAGAGCTTTGCTGTGGTCTGTGATGATGATGC 960
QY 961 CAAATCTGCTGCGGGAACAAACAGATGATGATGCTTAAACAGAGATCCTGTA 1020
  
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DB 961 CAAATCTGCTGCGGGAACAAACAGATGATGATGCTTAAACAGAGATCCTGTA 1020
QY 1021 ATGGGATATGAGCAATGTTTCCAGACAAAGCGCTAATATCTGATAGAGACATTAATA 1080
DB 1021 ATGGGATATGAGCAATGTTTCCAGACAAAGCGCTAATATCTGATAGAGACATTAATA 1080
QY 1081 GATTTGATGAGATTTATGTCGCAACCTTGATGGCTATCACTTCAACTGAATTTGA 1140
DB 1081 GATTTGATGAGATTTATGTCGCAACCTTGATGGCTATCACTTCAACTGAATTTGA 1140
QY 1141 CCCAGAACTACTTTTCAACAAATTCAGATCAACAAATGATATGCTGTGAATTTAA 1200
DB 1141 CCCAGAACTACTTTTCAACAAATTCAGATCAACAAATGATATGCTGTGAATTTAA 1200
QY 1201 CACCTCTATCTACCTGCAATCCCTCTGCTGCAACCTTTGAATTCAGACAGAAATA 1260
DB 1201 CACCTCTATCTACCTGCAATCCCTCTGCTGCAACCTTTGAATTCAGACAGAAATA 1260
QY 1261 CAACTATCAACAGTTATCTACACAACTCTATATTTGCTGGAACATGGAATTAACCA 1320
DB 1261 CAACTATCAACAGTTATCTACACAACTCTATATTTGCTGGAACATGGAATTAACCA 1320
QY 1321 TGTGATATCTTACACAGCAATTTGCTGGCAGGCTGCTGGTGTGAGAAATGTTCCACC 1380
DB 1321 TGTGATATCTTACACAGCAATTTGCTGGCAGGCTGCTGGTGTGAGAAATGTTCCACC 1380
QY 1381 CGCAGTACAGAAAGTATCAACAGCTTCCATTCACAGACAGACAGAGATGAATACAGTC 1440
DB 1381 CGCAGTACAGAAAGTATCAACAGCTTCCATTCACAGACAGACAGATGAATACAGTC 1440
QY 1441 TTTTAAATGATCCGCAACGCTTTATGCTGGAAGCCCTTATGAATCAATTTGAACCTTAC 1500
DB 1441 TTTTAAATGATCCGCAACGCTTTATGCTGGAAGCCCTTATGAATCAATTTGAACCTTAC 1500
QY 1501 AGAGAGAAAGAAATGTCTGACAGATTGGAAGACCTTATGCTGATGATGCTGTGGA 1560
DB 1501 AGAGAGAAAGAAATGTCTGACAGATTGGAAGACCTTATGCTGATGATGCTGTGGA 1560
QY 1561 GCTGTATCTGCGCTTCTGTGTGAAGAGCTGGGCGAGATGCGATCTTTGGTGAACAT 1620
DB 1561 GCTGTATCTGCGCTTCTGTGTGAAGAGCTGGGCGAGATGCGATCTTTGGTGAACAT 1620
QY 1621 GGTAGAAGTTGAGACCACTTCTCTTGAAGAGCTTATGGGTATGTTATGTTCTCC 1680
DB 1621 GGTAGAAGTTGAGACCACTTCTCTTGAAGAGCTTATGGGTATGTTATGTTCTCC 1680
QY 1681 TGCCTATCTGAAAGCCAGACATTTTGTGTGAGAGATGGGTTTCAATCATCAACTGC 1740
DB 1681 TGCCTATCTGAAAGCCAGACATTTTGTGTGAGAGATGGGTTTCAATCATCAACTGC 1740
QY 1741 CTCATTTAGTCTCTCATCTGCAATTAAGTGAAGGAGCTGCTTACTTACTTCACTGAT 1800
DB 1741 CTCATTTAGTCTCTCATCTGCAATTAAGTGAAGGAGCTGCTTACTTACTTCACTGAT 1800
QY 1801 TCCAGATCCAGAGCTCATTAATAACAGTCAACATCAATGCAAGTTCTTCCGCTCCGGA 1860
DB 1801 TCCAGATCCAGAGCTCATTAATAACAGTCAACATCAATGCAAGTTCTTCCGCTCCGGA 1860
QY 1861 AGATGATATCAATCCCAAGTACTACTTAAAGAAAGGCTGACCTGAACCTGAGAGGCTTAA 1920
DB 1861 AGATGATATCAATCCCAAGTACTACTTAAAGAAAGGCTGACCTGAACCTGAGAGGCTTAA 1920
QY 1921 TGAATCATTTATTTATATATGAACATGCTATTAATTAATTAATTAATTAATTAATTA 1980
DB 1921 TGAATCATTTATTTATATATGAACATGCTATTAATTAATTAATTAATTAATTAATTA 1980
QY 1981 ATATTAACCTCTTATATGTTACTTATCACTTCTGTAACAGAGTCTGATCTCTGTGG 2040
DB 1981 ATATTAACCTCTTATATGTTACTTATCACTTCTGTAACAGAGTCTGATCTCTGTGG 2040
QY 2041 GAGAAAGAGTCAATCTTGTGAAGACTTTTATGCTCACTCTTAAGATTTTGTGTGC 2100
DB 2041 GAGAAAGAGTCAATCTTGTGAAGACTTTTATGCTCACTCTTAAGATTTTGTGTGC 2100
  
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QY 2101 TGTAGTTTGGAAAAAGTTTATTTCTGTTTATTAACCAAGAGAAATGAGTTTGA 2160
DB 2101 TGTAAAGTTTGGAAAAAGTTTATTTCTGTTTATTAACCAAGAGAAATGAGTTTGA 2160
QY 2161 CGCTTTTACTTGAATTTCACTTATTAATTAAGAGCAAAAGTAAAGTGTGAAATAC 2220
DB 2161 CGCTTTTACTTGAATTTCACTTATTAATTAAGAGCAAAAGTAAAGTGTGAAATAC 2220
QY 2221 TTAACACATATACCAAGATGCCAAAATGCTGAAAGTTTTCACCTGCACTGTTCCAT 2280
DB 2221 TTAACACATATACCAAGATGCCAAAATGCTGAAAGTTTTCACCTGCACTGTTCCAT 2280
QY 2281 GGAATCTTCATGATGATTGAAGTAACTAATGTTGAAATTTTAAAGTCTTTGGGTA 2340
DB 2281 GGAATCTTCATGATGATTGAAGTAACTAATGTTGAAATTTTAAAGTCTTTGGGTA 2340
QY 2341 TTTTCTGTCATCAAAACAAAACAGGATACGATGATTAATTAATGAATTTTAATTTGA 2400
DB 2341 TTTTCTGTCATCAAAACAAAACAGGATACGATGATTAATTAATGAATTTTAATTTGA 2400
QY 2401 CATTAACAGTAATTTTCACTGCTTCTTAAATGCAATGAAACAAATATTTGAAAT 2460
DB 2401 CATTAACAGTAATTTTCACTGCTTCTTAAATGCAATGAAACAAATATTTGAAAT 2460
QY 2461 TCTAATTCATGAGGTAGATACCTGTAAAGCTTTGTTGATTTCTTAAAGTTTAA 2520
DB 2461 TCTAATTCATGAGGTAGATACCTGTAAAGCTTTGTTGATTTCTTAAAGTTTAA 2520
QY 2521 CTGTAACATATACCAAAAGAAAGCTGCTGATGATTAATCTGTAAATCAGATGAAAT 2580
DB 2521 CTGTAACATATACCAAAAGAAAGCTGCTGATGATTAATCTGTAAATCAGATGAAAT 2580
QY 2581 TTACTACAAATGCTGTTTAAATATTTTAAATGATGATGCTTTTCCACCAAGATTA 2640
DB 2581 TTACTACAAATGCTGTTTAAATATTTTAAATGATGATGCTTTTCCACCAAGATTA 2640
QY 2641 AAACCTTTTATGATGATGCTTTAAATCTGTTTAAATCAAAATGCCAAATTTTAAAG 2700
DB 2641 AAACCTTTTATGATGATGCTTTAAATCTGTTTAAATCAAAATGCCAAATTTTAAAG 2700
QY 2701 TGTGAGAGCCACTGAGTGTATCTCAAAATTAAGATTCCTGTTGAGATATTCAGAT 2760
DB 2701 TGTGAGAGCCACTGAGTGTATCTCAAAATTAAGATTCCTGTTGAGATATTCAGAT 2760
QY 2761 CTGTTTATATGCTGTGTAACATGTAATAAACCCCATTAACCCCGCCAAAAGGGTCTTACC 2820
DB 2761 CTGTTTATATGCTGTGTAACATGTAATAAACCCCATTAACCCCGCCAAAAGGGTCTTACC 2820
QY 2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATGTTGCCAAATTTAGGGT 2880
DB 2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATGTTGCCAAATTTAGGGT 2880
QY 2881 TTAACCTTTTGAAGCAAACTTTTGTAGCTGTGCACTGCACTGCTGATCAGAT 2940
DB 2881 TTAACCTTTTGAAGCAAACTTTTGTAGCTGTGCACTGCACTGCTGATCAGAT 2940
QY 2941 TTTGCTATGAGGTTAATGAAGTACCAAGCTGTGCTTAATTAACGATGTTTCTGAT 3000
DB 2941 TTTGCTATGAGGTTAATGAAGTACCAAGCTGTGCTTAATTAACGATGTTTCTGAT 3000
QY 3001 TTTTCTGTTGACGTTTAAATTTAGCAGTCCATATCAGATTTGCAAAAGTAGACATC 3060
DB 3001 TTTTCTGTTGACGTTTAAATTTAGCAGTCCATATCAGATTTGCAAAAGTAGACATC 3060
QY 3061 ATAAATATACCTCTCAAAATGCTTAATATGATTCACATTAATTTTATCTAGTCTG 3120
DB 3061 ATAAATATACCTCTCAAAATGCTTAATATGATTCACATTAATTTTATCTAGTCTG 3120
QY 3121 AAGCAATTCAGTAGTGAATGCAATCAAGCTGCTGATCAGTCTGCTTTCT 3180
DB 3121 AAGCAATTCAGTAGTGAATGCAATCAAGCTGCTGATCAGTCTGCTTTCT 3180

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QY 3181 TTTCTCTTTTAGCCATTTTGGTAAAGACACAGCTCTCTCAAAAGCTTCTTCTCTA 3240
DB 3181 TTTCTCTTTTAGCCATTTTGGTAAAGACACAGCTCTCTCAAAAGCTTCTTCTCTA 3240
QY 3241 TTTTGTTTTACTAGTTTAAAGATCAGAGTTCATCTTCTTGGACTGACCTATTTCT 3300
DB 3241 TTTTGTTTTACTAGTTTAAAGATCAGAGTTCATCTTCTTGGACTGACCTATTTCT 3300
QY 3301 TACCTGAACTTTTGCAGTTTTCAGGTAAACCTCAGCTCAGAGACTGCTATTTAGCTCTC 3360
DB 3301 TACCTGAACTTTTGCAGTTTTCAGGTAAACCTCAGCTCAGAGACTGCTATTTAGCTCTC 3360
QY 3361 TTAAGAGATTAATAAAAAAAAAAAG 3387
DB 3361 TTAAGAGATTAATAAAAAAAAAAAG 3387

RESULT 2
AAQ71002
ID AAQ71002 standard; cDNA; 3387 BP.
XX
AC AAQ71002;
XX
AC 25-MAR-2003 (revised)
DT 27-FEB-1995 (first entry)
XX
DE Cyclooxygenase-2 cDNA.
XX
KM Cyclooxygenase-2; enzyme; osteosarcoma; assay; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 57..1910
FT /tag= a
FT /label= cyclooxygenase-2
XX
XX W09414977-A1.
XX
XX 07-JUL-1994.
XX
XX 17-DEC-1993; 93WO-CA000547.
XX
XX 22-DEC-1992; 92US-00994760.
XX
XX 06-MAY-1993; 93US-00064271.
XX
XX (MERI ) MERCK FROST CANADA INC.
XX
XX Cromlish WA, Kennedy BP, Oneill G, Vickers PJ, Wong E;
XX
XX Mancini JA;
XX
XX WPI; 1994-263635/32.
XX
XX P-PSDB; AAR56660.
XX
XX Assays for cyclo-oxygenase-1 and -2 - for identifying selective
XX
XX antagonists, i.e. potential anti inflammatory etc., also new human
XX
XX cyclo-oxygenase-2 and cDNA encoding it.
XX
XX Disclosure; Fig 2A-2C; 55pp; English.
XX
XX The human cyclooxygenase-2 cDNA is isolated from osteosarcoma cells, and
XX
XX is expressed from a mammalian or eukaryotic vector. The COX-2 protein is
XX
XX used in assays to identify inhibitors which have antiinflammatory,
XX
XX antipyretic, analgesic and anticancer activity. (Updated on 25-MAR-2003
XX
XX to correct FN field.)
XX
XX
XX Sequence 3387 BP; 1010 A; 715 C; 631 G; 1031 T; 0 U; 0 Other;
XX
XX
XX Query Match 99.8%; Score 3380.6; DB 2; Length 3387;
XX
XX Best Local Similarity 99.9%; Pred. No. 0;
XX
XX Matches 3383; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 GTCAGGAACCTCTCAGCAGCGCTCTTCACTCAGCTCCAGCCGAGCGCCCTCAGACGCA 60

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Db 1 GTCCAGGAACCTCCACGAGCGCCCTCCCTTCAGCTCCACAGCCAAACGCGCTTCAACAGCA 60
QY AAGCTTACCCCGGCGCGCGCGCTCCCGCGCGCTGCATGTCTCGCGCGCGCTGTCTCT 120
Db 61 AAGCTTACCCCGGCGCGCGCGCTCCCGCGCGCTGCATGTCTCGCGCGCGCTGTCTCT 120
QY 121 GTGCGCGGTCTCTGCGCTCAGCCCAATGCAAAATCTCTGTTCCACCCATGTCAAAA 180
Db 121 GTGCGCGGTCTCTGCGCTCAGCCCAATGCAAAATCTCTGTTCCACCCATGTCAAAA 180
QY 181 CCGAGGTGTATGTATGATGTGTGGATTTGACAGATATAGTGCATTTGACCCGGAAG 240
Db 181 CCGAGGTGTATGTATGATGTGTGGATTTGACAGATATAGTGCATTTGACCCGGAAG 240
QY 241 ATTCTATGAGAAAACTGCTCAACACCGGAAATTTTGAAGAATTAATTAATTTCTGAA 300
Db 241 ATTCTATGAGAAAACTGCTCAACACCGGAAATTTTGAAGAATTAATTAATTTCTGAA 300
QY 301 ACCCACTCCAAACACAGTGCATCATCTTACCACTTCAAGGGAATTTTGAAGTTGT 360
Db 301 ACCCACTCCAAACACAGTGCATCATCTTACCACTTCAAGGGAATTTTGAAGTTGT 360
QY 361 GAATTAACATTCCTCTCTTCCGAATGCAATTAATGATTAATGTGATGATCCAGATCACA 420
Db 361 GAATTAACATTCCTCTCTTCCGAATGCAATTAATGATTAATGTGATGATCCAGATCACA 420
QY 421 TTTGATGACAGTCCACCACTTACATGCTGACTAGTGGCTACAAAGCTGGGAAGCTT 480
Db 421 TTTGATGACAGTCCACCACTTACATGCTGACTAGTGGCTACAAAGCTGGGAAGCTT 480
QY 481 CTCTAACCTCTCTATTAATTAATGAGCCCTTCTCTGCTGATGATGTGCGCAATCC 540
Db 481 CTCTAACCTCTCTATTAATTAATGAGCCCTTCTCTGCTGATGATGTGCGCAATCC 540
QY 541 CTGAGCTCTCTCTATTAATTAATGAGCCCTTCTCTGCTGATGATGTGCGCAATCC 540
Db 541 CTGAGCTCTCTCTATTAATTAATGAGCCCTTCTCTGCTGATGATGTGCGCAATCC 540
QY 541 CTGAGCTCTCTCTATTAATTAATGAGCCCTTCTCTGCTGATGATGTGCGCAATCC 540
Db 541 CTGAGCTCTCTCTATTAATTAATGAGCCCTTCTCTGCTGATGATGTGCGCAATCC 540
QY 601 TCTAAGAAAGAAATTCATCCCTGATCCCAAGGCTCAAAATGATGTGCTTCTTGC 660
Db 601 TCTAAGAAAGAAATTCATCCCTGATCCCAAGGCTCAAAATGATGTGCTTCTTGC 660
QY 661 CCAGCACTTCAAGCAGCTTTTCAAGCAGATCATAGCGAGGGCGCTTCAACCA 720
Db 661 CCAGCACTTCAAGCAGCTTTTCAAGCAGATCATAGCGAGGGCGCTTCAACCA 720
QY 721 CGGGCTGGGCGCAATGGGGTGAATTAATGATTAATGATTAATGATTAATGATTAATG 780
Db 721 CGGGCTGGGCGCAATGGGGTGAATTAATGATTAATGATTAATGATTAATGATTAATG 780
QY 781 TAAATGCGCTCTTTCAGAGATGAGAAAAATGAATATCAGATTAATGATGAGAGATGA 840
Db 781 TAAATGCGCTCTTTCAGAGATGAGAAAAATGAATATCAGATTAATGATGAGAGATGA 840
QY 841 TCTCTCCACAGTGAAGATTAATCAGGCAAGATGATTAATCCTTCCCAAGTCCCTGAGA 900
Db 841 TCTCTCCACAGTGAAGATTAATCAGGCAAGATGATTAATCCTTCCCAAGTCCCTGAGA 900
QY 901 TCTAAGCTTGTGCTGGGCGAGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 TCTAAGCTTGTGCTGGGCGAGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 CACAAATCTGGCTCGGGAACACAAACAGATATGATGATGATTAATCAGAGGATCTGA 1020
Db 961 CACAAATCTGGCTCGGGAACACAAACAGATATGATGATGATTAATCAGAGGATCTGA 1020
QY 1021 ATGGGGTGTAGACAGTGTGTTCAAGACAGAGGCTTAATCTGATGAGAGACATTTAA 1080
Db 1021 ATGGGGTGTAGACAGTGTGTTCAAGACAGAGGCTTAATCTGATGAGAGACATTTAA 1080
QY 1081 GATTGATTGAAGATTATGTCACACTGAGTGGCTATCATTTCAAACTGAAATTTGA 1140

Db 1081 GATTGATTGAAGATTATGTCACACTGAGTGGCTATCATTTCAAACTGAAATTTGA 1140
QY 1141 CCGAGAACTACTTTTCAACAAACATTCAGATACCAAAATGATATGCTGTGAATTTAA 1200
Db 1141 CCGAGAACTACTTTTCAACAAACATTCAGATACCAAAATGATATGCTGTGAATTTAA 1200
QY 1201 CACCTCTATCAGTGGCAATCCCTTCTGCGCAGACACTTTCAAATGATGACGAAATA 1260
Db 1201 CACCTCTATCAGTGGCAATCCCTTCTGCGCAGACACTTTCAAATGATGACGAAATA 1260
QY 1261 CAACTATCAACAGTTTATCTAACAACCTATATGCTGGAACATGAAATTTACCAAT 1320
Db 1261 CAACTATCAACAGTTTATCTAACAACCTATATGCTGGAACATGAAATTTACCAAT 1320
QY 1321 TGTGAAATCATTCACAGGCAAAATGCTGGAAGGTTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 1321 TGTGAAATCATTCACAGGCAAAATGCTGGAAGGTTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1381 CGCAGTACAGAAAGATACAGAGCTTCATTTGACAGAGCAGAGAGATGAATACAGTTC 1440
Db 1381 CGCAGTACAGAAAGATACAGAGCTTCATTTGACAGAGCAGAGAGATGAATACAGTTC 1440
QY 1441 TTTTATGAGTACCGCAAAAGCTTTATGCTGAAGCTTATGATCATTTGAAAGACTTAC 1500
Db 1441 TTTTATGAGTACCGCAAAAGCTTTATGCTGAAGCTTATGATCATTTGAAAGACTTAC 1500
QY 1501 AGGAAAGAAAGAAATGCTGGAAGGTTGGAAGCACTTATGCTGATCATGAGTGTGGA 1560
Db 1501 AGGAAAGAAAGAAATGCTGGAAGGTTGGAAGCACTTATGCTGATCATGAGTGTGGA 1560
QY 1561 GCTGATCTGCTCTCTCTGATGAGAAAGCTTCGCGCAGATGCAATCTTTGTGAAACCAT 1620
Db 1561 GCTGATCTGCTCTCTCTGATGAGAAAGCTTCGCGCAGATGCAATCTTTGTGAAACCAT 1620
QY 1621 GGTAGAGTGGAGCAACATCTCTTGAAGAGCTTATGCTGATGATGATGATGATGATG 1680
Db 1621 GGTAGAGTGGAGCAACATCTCTTGAAGAGCTTATGCTGATGATGATGATGATGATG 1680
QY 1681 TCCCTACCTGGAAGCCAGAGCACTTTGTGGAAGAGTGGGTTTCAATCATACACATG 1740
Db 1681 TCCCTACCTGGAAGCCAGAGCACTTTGTGGAAGAGTGGGTTTCAATCATACACATG 1740
QY 1741 CTCAATGAGTCTCATCTGCAATGAGTGAAGGCTGCTTCTTCACTTCACTGATG 1800
Db 1741 CTCAATGAGTCTCATCTGCAATGAGTGAAGGCTGCTTCTTCACTTCACTGATG 1800
QY 1801 TCCAGATCCAGCTCATTTAAACAGTCCATCAATGCAAGTCTTCCGCTCGGAGCT 1860
Db 1801 TCCAGATCCAGCTCATTTAAACAGTCCATCAATGCAAGTCTTCCGCTCGGAGCT 1860
QY 1861 AGATGATATCATCCACAGTCTACTTAAAGACGCTGCACTGAACCTGAGAGCTTAA 1920
Db 1861 AGATGATATCATCCACAGTCTACTTAAAGACGCTGCACTGAACCTGAGAGCTTAA 1920
QY 1921 TGAATATTTATTTATTTATTAAGAACATGCTATTAATTTATTAATTTATTAATTT 1980
Db 1921 TGAATATTTATTTATTTATTAAGAACATGCTATTAATTTATTAATTTATTAATTT 1980
QY 1981 ATATTAATCTCTTATGTTATTAATTAATCTGTAACAGAGTCACTCTCTGTTGG 2040
Db 1981 ATATTAATCTCTTATGTTATTAATTAATCTGTAACAGAGTCACTCTCTGTTGG 2040
QY 2041 GAGAAAGAGTCAATCTTGAAGACTTTATGCTCACTACTTAAGATTTTGTCTGTTG 2100
Db 2041 GAGAAAGAGTCAATCTTGAAGACTTTATGCTCACTACTTAAGATTTTGTCTGTTG 2100
QY 2101 TGTTAAGTTTGAAGAAAGCTTTTATCTGTTTATTAACAGAGAAATGAGTTTGA 2160
Db 2101 TGTTAAGTTTGAAGAAAGCTTTTATCTGTTTATTAACAGAGAAATGAGTTTGA 2160
QY 2161 CGTCTTTTATCTTGAATTTCAACTTATTAATTAATTAAGACGAAATGATGATGATG 2220
Db 2161 CGTCTTTTATCTTGAATTTCAACTTATTAATTAATTAAGACGAAATGATGATGATG 2220

QY 2221 TTAAACGATATCAAGAGATCCAAAATGCTGAAGTTTTCACCTGTCAGTGTTCAT 2280
 DB 2221 TTAAACGATATCAAGAGATCCAAAATGCTGAAGTTTTCACCTGTCAGTGTTCAT 2280
 QY 2281 GCATCTCCGATGATGATTAAGATTAATGTTGAATTTTAAAGTACTTTGGGTA 2340
 DB 2281 GCATCTCCGATGATGATTAAGATTAATGTTGAATTTTAAAGTACTTTGGGTA 2340
 QY 2341 TTTTCTGTCATCAAAAACAGATATCATGTCATTTAATTAATTAATTAATTAATTA 2400
 DB 2341 TTTTCTGTCATCAAAAACAGATATCATGTCATTTAATTAATTAATTAATTAATTA 2400
 QY 2401 CATTAACGATTAATTCATGTCATTTTAAATCAAGCAATGAATTAATTTGAAT 2460
 DB 2401 CATTAACGATTAATTCATGTCATTTTAAATCAAGCAATGAATTAATTTGAAT 2460
 QY 2461 TCTAAATTCATGAGGATGATGATCACTGTAAGAGCTGTTGATTTCTTAAAGTTATA 2520
 DB 2461 TCTAAATTCATGAGGATGATGATCACTGTAAGAGCTGTTGATTTCTTAAAGTTATA 2520
 QY 2521 CTGTGACATATACCAAAAAGAGCTGCTGTGATTTAAATCTGTAAATCAGATGAAT 2580
 DB 2521 CTGTGACATATACCAAAAAGAGCTGCTGTGATTTAAATCTGTAAATCAGATGAAT 2580
 QY 2581 TTACTACATTTGCTGTTTAAATATTTTAAAGATGTTCTTTTCAACAAGATATA 2640
 DB 2581 TTACTACATTTGCTGTTTAAATATTTTAAAGATGTTCTTTTCAACAAGATATA 2640
 QY 2641 AACCTTTTAAAGTACGCTGTTAAATCTCTTTTAAATCAAAATGCAATTTTAAAG 2700
 DB 2641 AACCTTTTAAAGTACGCTGTTAAATCTCTTTTAAATCAAAATGCAATTTTAAAG 2700
 QY 2701 TGGTGAAGCAGCTGACAGTGTATCTCAAAATAGAAATATCTGTTGAGATTTTCAAGAT 2760
 DB 2701 TGGTGAAGCAGCTGACAGTGTATCTCAAAATAGAAATATCTGTTGAGATTTTCAAGAT 2760
 QY 2761 CTGTTTATATGCTGCTGATACATGTAAAAAAGCTGTTGAGATTTTCAAGAT 2820
 DB 2761 CTGTTTATATGCTGCTGATACATGTAAAAAAGCTGTTGAGATTTTCAAGAT 2820
 QY 2821 TTGAACATTAAGCATTAAACCAAGAGAAAGCCCAATTAATTTGTTTCAATTTAGGAT 2880
 DB 2821 TTGAACATTAAGCATTAAACCAAGAGAAAGCCCAATTAATTTGTTTCAATTTAGGAT 2880
 QY 2881 TTAAACCTTTTGAAGCAAACTTTTGTAGCTGTCAGACCTGATACCTGAT 2940
 DB 2881 TTAAACCTTTTGAAGCAAACTTTTGTAGCTGTCAGACCTGATACCTGAT 2940
 QY 2941 TTTGCTATGAGGTTAATGAAATGACCAAGCTGTTGATTAATGATTTTTCAGAT 3000
 DB 2941 TTTGCTATGAGGTTAATGAAATGACCAAGCTGTTGATTAATGATTTTTCAGAT 3000
 QY 3001 TTTGCTGTAAGGTTAATTAAGAGTCCATATACATTTGTAAGTAAGTACATACCTC 3060
 DB 3001 TTTGCTGTAAGGTTAATTAAGAGTCCATATACATTTGTAAGTAAGTACATACCTC 3060
 QY 3061 ATAAATATGCTCTTCAAAATGCTTAATTAATTCATTTCAACATTTAATTCAGTCTG 3120
 DB 3061 ATAAATATGCTCTTCAAAATGCTTAATTAATTCATTTCAACATTTAATTCAGTCTG 3120
 QY 3121 AAGCCAAATTCAGTATGATGATTAAGATCAAGCTGATACCTGATGCTGTTCTTCT 3180
 DB 3121 AAGCCAAATTCAGTATGATGATTAAGATCAAGCTGATACCTGATGCTGTTCTTCT 3180
 QY 3181 TTTCTCTCTTTAGCAATTTGTTAAGAGACAGCTCTTCTCAAAACATTTGTTCTCTTA 3240
 DB 3181 TTTCTCTCTTTAGCAATTTGTTAAGAGACAGCTCTTCTCAAAACATTTGTTCTCTTA 3240
 QY 3241 TTTGTTTACTAGTTTAAATGATGAGATCACTTTTGGAGCTGCTGATTAATTTCT 3300
 DB 3241 TTTGTTTACTAGTTTAAATGATGAGATCACTTTTGGAGCTGCTGATTAATTTCT 3300

QY 3301 TACTGAACCTTTTGAAGTTTTCAGSTAAACCTCAGCTCAGATCTGATTTAGTCTTC 3360
 DB 3301 TACTGAACCTTTTGAAGTTTTCAGSTAAACCTCAGCTCAGATCTGATTTAGTCTTC 3360
 QY 3361 TTAAAGAGATTAATAAAAAAAAAAAAAAG 3387
 DB 3361 TTAAAGAGATTAATAAAAAAAAAAAAAAG 3387
 RESULT 3
 AAA34993
 ID AAA34993 standard; DNA; 3387 BP.
 XX
 AC AAA34993;
 XX
 DT 28-UTL-2000 (first entry)
 XX
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2682.
 DE
 XX Human: adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
 KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US017712.
 XX
 PR 03-AUG-1998; 98US-0095212P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JM;
 XX
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Disclosure; Page 890-891; 1343pp; English.
 XX
 The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cyostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.

CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO. sequences given in the sequence
CC listing

XX Sequence 3387 BP; 1010 A; 712 C; 633 G; 1032 T; 0 U; 0 Other;

Query Match 99.8%; Score 3379; DB 3; Length 3387;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 GTCCAGGAATCTCTCAGCAGCGCTCTCTCACTCCACAGCCAGAGCCCTCAGACAGCA 60
DB 1 GTCCAGGAATCTCTCAGCAGCGCTCTCTCACTCCACAGCCAGAGCCCTCAGACAGCA 60
QY 61 AAGCCTACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 61 AAGCCTACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 GTGCGCGGTCTGCGCGCTCAGCCATACAGCAAAATCCTTGCTGTCACCACTGTCAAA 180
DB 121 GTGCGCGGTCTGCGCGCTCAGCCATACAGCAAAATCCTTGCTGTCACCACTGTCAAA 180
QY 181 CGAGAGTATATATATATATATATATATATATATATATATATATATATATATATAT 240
DB 181 CGAGAGTATATATATATATATATATATATATATATATATATATATATATATATAT 240
QY 241 ATTCTATGAGAAATCTGTCAAACCGGAAATTTTGAACAAGATTAATTTCTGAA 300
DB 241 ATTCTATGAGAAATCTGTCAAACCGGAAATTTTGAACAAGATTAATTTCTGAA 300
QY 301 ACCCACTCCAAACACAGTGCATACATACCTTACCCACTTCAAGGAGTTTGGAACTGT 360
DB 301 ACCCACTCCAAACACAGTGCATACATACCTTACCCACTTCAAGGAGTTTGGAACTGT 360
QY 361 GAATAACATTTCCCTCTCTCGAAATGCAATATATATATATATATATATATATATAT 420
DB 361 GAATAACATTTCCCTCTCTCGAAATGCAATATATATATATATATATATATATATAT 420
QY 421 TTGTATGACAGTCCCAACTTGAATGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 TTGTATGACAGTCCCAACTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 CTCTAACCTCTCTCTATTAATAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
DB 481 CTCTAACCTCTCTCTATTAATAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 541 CTCTGAGTGTCAAAAGTAAAGAGAGCTCTCTGATTCAAATGAGATTTGGGAAATTTGCT 600
DB 541 CTCTGAGTGTCAAAAGTAAAGAGAGCTCTCTGATTCAAATGAGATTTGGGAAATTTGCT 600
QY 601 TCTTAAGAGAAATGTCATCCCTGATCCCAAGGCTCAAAATGATGTTGCTCTCTCTG 660
DB 601 TCTTAAGAGAAATGTCATCCCTGATCCCAAGGCTCAAAATGATGTTGCTCTCTCTG 660
QY 661 CCAGCATTCACGATCAATTTTCAAGACATTAAGCGAGGCGAGCTTTCACAA 720
DB 661 CCAGCATTCACGATCAATTTTCAAGACATTAAGCGAGGCGAGCTTTCACAA 720
QY 721 CGGCGTGGCGCATGGGCTGATTAATCATATTTACGTTGAACTCTGGCTGACAGCG 780
DB 721 CGGCGTGGCGCATGGGCTGATTAATCATATTTACGTTGAACTCTGGCTGACAGCG 780
QY 781 TAAACTGCGCTTTTCAAGAGTGAATAATGAAATATCAGATTAATGATGAAGATGA 840
DB 781 TAAACTGCGCTTTTCAAGAGTGAATAATGAAATATCAGATTAATGATGAAGATGA 840
QY 841 TCTCTCCACAGTCAAAAGATCTCAGGCAAGATGATCTACCTCTCAAGTCTCTGAGCA 900
DB 841 TCTCTCCACAGTCAAAAGATCTCAGGCAAGATGATCTACCTCTCAAGTCTCTGAGCA 900
QY 901 TCTACGTTTGTCTGTGGGCGAGAGGTTCTTGTGCTGTGGTCTGTGATGATGTC 960
DB 901 TCTACGTTTGTCTGTGGGCGAGAGGTTCTTGTGCTGTGGTCTGTGATGATGTC 960
```

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QY 961 CACAACTGTGGTGGGGAACAACAAGATATGATGCTTAAACAGAGATCTCTGA 1020
DB 961 CACAACTGTGGTGGGGAACAACAAGATATGCAATGTGCTTAAACAGAGATCTCTGA 1020
QY 1021 ATGGGGTATGAGCAGTTGTTCCAGACAGAGCTAATCTGATGAGAGACTATTA 1080
DB 1021 ATGGGGTATGAGCAGTTGTTCCAGACAGAGCTAATCTGATGAGAGACTATTA 1080
QY 1081 GATTGTGATGAAAGTTATGAGCAACTTGAAGGCTATCACTTCAAACTGAATTTGA 1140
DB 1081 GATTGTGATGAAAGTTATGAGCAACTTGAAGGCTATCACTTCAAACTGAATTTGA 1140
QY 1141 CCCAGAACTACTTTTCAACAAATTCAGTACCAAAATGATATGCTGCTGAATTTAA 1200
DB 1141 CCCAGAACTACTTTTCAACAAATTCAGTACCAAAATGATATGCTGCTGAATTTAA 1200
QY 1201 CACCTCTATCAGTGGCATCCCTCTCTGCTGACACTTTCAATTCATGACCAAAAT 1260
DB 1201 CACCTCTATCAGTGGCATCCCTCTCTGCTGACACTTTCAATTCATGACCAAAAT 1260
QY 1261 CAACATCAACAGTTATCTACACACACTATATATGCTGGAACAGAAATACCAAT 1320
DB 1261 CAACATCAACAGTTATCTACACACACTATATATGCTGGAACAGAAATACCAAT 1320
QY 1321 TGTGATCATTCACACAGCAATTTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 TGTGATCATTCACACAGCAATTTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 CGCAGTACAGAAAGTATCAGAGCTTCCATATGACACAGACAGAGCTAATACAGTC 1440
DB 1381 CGCAGTACAGAAAGTATCAGAGCTTCCATATGACACAGACAGAGCTAATACAGTC 1440
QY 1441 TTTTATGATGATCCGAAACGCTTATGCTGAAGCCCTATGATCAATTTGAAGAACTTAC 1500
DB 1441 TTTTATGATGATCCGAAACGCTTATGCTGAAGCCCTATGATCAATTTGAAGAACTTAC 1500
QY 1501 AGAGAGAAAGAAATGTGACAGAGTGGAAACACTATATGATGATGATGCTGTGA 1560
DB 1501 AGAGAGAAAGAAATGTGACAGAGTGGAAACACTATATGATGATGATGCTGTGA 1560
QY 1561 GCTGATCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 GCTGATCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 GGTAGAGTTGAGACCAATCTCTCTGAAAGCACTTATGAGGTAATGTTATGTTCTCC 1680
DB 1621 GGTAGAGTTGAGACCAATCTCTCTGAAAGCACTTATGAGGTAATGTTATGTTCTCC 1680
QY 1681 TGCCTAATGGAAGCCAGCACTTTTGTGAGAAAGTGGGTTTCAAAATCATCAACA 1740
DB 1681 TGCCTAATGGAAGCCAGCACTTTTGTGAGAAAGTGGGTTTCAAAATCATCAACA 1740
QY 1741 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGCTCTCTCTCTCTCTCTCT 1800
DB 1741 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGCTCTCTCTCTCTCTCTCT 1800
QY 1801 TCCAGATCCAGAGCTCATTAACAGTCAACATCAATGCAAGTTCTTCCGCTCGGAGCT 1860
DB 1801 TCCAGATCCAGAGCTCATTAACAGTCAACATCAATGCAAGTTCTTCCGCTCGGAGCT 1860
QY 1861 AGATGATATCAATCCCAAGTACTTAAAGAAAGAGTTCAGAGAACTGAGAGTCTAA 1920
DB 1861 AGATGATATCAATCCCAAGTACTTAAAGAAAGAGTTCAGAGAACTGAGAGTCTAA 1920
QY 1921 TGAATATATATATATATATATATATATATATATATATATATATATATATATAT 1980
DB 1921 TGAATATATATATATATATATATATATATATATATATATATATATATATATAT 1980
QY 1981 ATATTAACCTCTTATGTTACTTAAATCATCTTCTGTAACAGAAATGATGATCTCTGTTGGC 2040
DB 1981 ATATTAACCTCTTATGTTACTTAAATCATCTTCTGTAACAGAAATGATGATCTCTGTTGGC 2040
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QY 2041 GAGAAAGAGTCACTGCTGAGAGCTTTTANGTCACTACTCTAAAGATTTTCTGCTGC 2100
 DB 2041 GAGAAAGAGTCACTGCTGAGAGCTTTTANGTCACTACTCTAAAGATTTTCTGCTGC 2100
 QY 2101 TGTAAAGTTGGAAAAAGTTTATTTCTGTTTATTAACCAAGAGAAATGCTTTGA 2160
 DB 2101 TGTAAAGTTGGAAAAAGTTTATTTCTGTTTATTAACCAAGAGAAATGCTTTGA 2160
 QY 2161 CGCTTTTACTGGAATTTCACTTAATTAAGAGCAAGAAAGTAAAGATGTTGAATAC 2220
 DB 2161 CGCTTTTACTGGAATTTCACTTAATTAAGAGCAAGAAAGTAAAGATGTTGAATAC 2220
 QY 2221 TTAACACTATACCAAGAGCCCAAAATGCTGAAAGTTTTCACCTGTCATGTTTCCAAT 2280
 DB 2221 TTAACACTATACCAAGAGCCCAAAATGCTGAAAGTTTTCACCTGTCATGTTTCCAAT 2280
 QY 2281 GCATCTTCATGATGATTAAGAAATGCTTAATGTTTGAATTTTAAAGTACTTTGGGTA 2340
 DB 2281 GCATCTTCATGATGATTAAGAAATGCTTAATGTTTGAATTTTAAAGTACTTTGGGTA 2340
 QY 2341 TTTTCTGTCATCAAAACAAACAGGTATGATGATTAATTAATGATTAATTAATTAAGA 2400
 DB 2341 TTTTCTGTCATCAAAACAAACAGGTATGATGATTAATTAATGATTAATTAATTAAGA 2400
 QY 2401 CATACACGATATTCATGCTCACTTTTAAATGAGCATGAAACATTAATTTGAAAT 2460
 DB 2401 CATACACGATATTCATGCTCACTTTTAAATGAGCATGAAACATTAATTTGAAAT 2460
 QY 2461 TCTAAATTCATAGGCTAGATCACTGTAAGAGCTTGTGTTGTTCTTAAAGTTTAA 2520
 DB 2461 TCTAAATTCATAGGCTAGATCACTGTAAGAGCTTGTGTTGTTCTTAAAGTTTAA 2520
 QY 2521 CTGTAACATATACCAAAAGAGCTGCTGTAATTAATCTGTAATCAAGATGAAAT 2580
 DB 2521 CTGTAACATATACCAAAAGAGCTGCTGTAATTAATCTGTAATCAAGATGAAAT 2580
 QY 2581 TTACACAAATGCTGTTTAAATTTTATTAAGATGTTCTTTTCAACCAAGATTA 2640
 DB 2581 TTACACAAATGCTGTTTAAATTTTATTAAGATGTTCTTTTCAACCAAGATTA 2640
 QY 2641 AACCTTTTATGATGATGTTTAAACTCTTTTAAATCAAAATGCCAAATTTTAAAG 2700
 DB 2641 AACCTTTTATGATGATGTTTAAACTCTTTTAAATCAAAATGCCAAATTTTAAAG 2700
 QY 2701 TGTGAGAGCACTGCACTGTTATCTCAAAATTAAGATATCTGTTGATATTCAGAAAT 2760
 DB 2701 TGTGAGAGCACTGCACTGTTATCTCAAAATTAAGATATCTGTTGATATTCAGAAAT 2760
 QY 2761 CTGTTTATGATGCTGTAACATGTAATAACCCCATACCCGCCAAAGGGGTCCTACCC 2820
 DB 2761 CTGTTTATGATGCTGTAACATGTAATAACCCCATACCCGCCAAAGGGGTCCTACCC 2820
 QY 2821 TTGAACATTAAGCATTAACCAAGGAGAAAGCCCAATTTATGTTTCCAAATTTAAGGT 2880
 DB 2821 TTGAACATTAAGCATTAACCAAGGAGAAAGCCCAATTTATGTTTCCAAATTTAAGGT 2880
 QY 2881 TTAACCTTTTGAAGCAAACTTTTATGCTTTGATGCTGAGAGCTGCTGATCAGAT 2940
 DB 2881 TTAACCTTTTGAAGCAAACTTTTATGCTTTGATGCTGAGAGCTGCTGATCAGAT 2940
 QY 2941 TTTGCTATGAGGTTAAAGAGTACCAAGCTGCTGTTAAATTAACATATGTTTCTCAGAT 3000
 DB 2941 TTTGCTATGAGGTTAAAGAGTACCAAGCTGCTGTTAAATTAACATATGTTTCTCAGAT 3000
 QY 3001 TTTCTGTTGATAGTTTAAATTTAGCAGTCACTATCACTTGCACAAAGATGACACTC 3060
 DB 3001 TTTCTGTTGATAGTTTAAATTTAGCAGTCACTATCACTTGCACAAAGATGACACTC 3060
 QY 3061 ATAAATTAACCTCTTCAAAATGCTTAAATTAATTAATTTATCTCAGCTGCTG 3120
 DB 3061 ATAAATTAACCTCTTCAAAATGCTTAAATTAATTAATTTATCTCAGCTGCTG 3120
 QY 3121 AAGCATTATAGTATGATGATGAAATCAAGCCGCTACCTGATGATGCTGCTTTCT 3180

DB 3121 AAGCATTATAGTATGATGAAATCAAGCCGCTACCTGATGATGCTGCTTTCT 3180
 QY 3181 TTTCTTTTATGACATTTTGTCTAAGAGACACAGTCTTCTCAACACTTCTTCTCTA 3240
 DB 3181 TTTCTTTTATGACATTTTGTCTAAGAGACACAGTCTTCTCAACACTTCTTCTCTA 3240
 QY 3241 TTTGTTTACTAGTTTAAAGATCAGAGTCACTTTCTTTGACTGCTGATATTTTCT 3300
 DB 3241 TTTGTTTACTAGTTTAAAGATCAGAGTCACTTTCTTTGACTGCTGATATTTTCT 3300
 QY 3301 TACCTGAACCTTTTGAAGTTTCAAGTAAACCTCAGCTCAGACCTGCTATTAAGCTCCTC 3360
 DB 3301 TACCTGAACCTTTTGAAGTTTCAAGTAAACCTCAGCTCAGACCTGCTATTAAGCTCCTC 3360
 QY 3361 TTAAGAGATTAATAAAAAAAAAAAG 3387
 DB 3361 TTAAGAGATTAATAAAAAAAAAAAG 3387

RESULT 4

AAE21115
ID AAE21115 standard; DNA; 3387 BP.

AAE21115;

14-MAR-2001 (first entry)

Human low adenosine antisense oligonucleotide related sequence #2682.

KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; se.

OS Homo sapiens.

PN WO200062736-A2.

BD 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

PR 06-APR-1999; 99US-0127958P.

PA (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

PI Nyce JW;

DR WPI; 2000-679539/66.

PT Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.

PS Disclosure; Page 965-966; 1592pp; English.

CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,

QY 1801 TCCAGATCCGAGCTCATTTAAACAGTACACATCATGCAAGTTCTTCCGCTCCGAGCT 1860
 Db 1801 TCCAGATCCGAGCTCATTTAAACAGTACACATCATGCAAGTTCTTCCGCTCCGAGCT 1860
 QY 1861 AGATGATATCAATCCCAAGTACTACTAAAGAAAGCGTGCATCGAACTGTAGAAAGTCTAA 1920
 Db 1861 AGATGATATCAATCCCAAGTACTACTAAAGAAAGCGTGCATCGAACTGTAGAAAGTCTAA 1920
 QY 1921 TGAATCATTTATTTATTTATATGAACCATGCTATTAATTAATTAATTAATTAATTAATTT 1980
 Db 1921 TGAATCATTTATTTATTTATATGAACCATGCTATTAATTAATTAATTAATTAATTAATTT 1980
 QY 1981 ATATTAACCTCTTATGTTACTTAACATCTTCTGTAACAGAAAGTCACTCTCTGTTGCG 2040
 Db 1981 ATATTAACCTCTTATGTTACTTAACATCTTCTGTAACAGAAAGTCACTCTCTGTTGCG 2040
 QY 2041 GAGAAAGAGTCATCTTGTGAAGACTTTATGTCATCTCTAAAGATTTTGTGCTGCTC 2100
 Db 2041 GAGAAAGAGTCATCTTGTGAAGACTTTATGTCATCTCTAAAGATTTTGTGCTGCTC 2100
 QY 2101 TGTAAAGTTTGAAAAACAGTTTATCTGTTTATTAACAGAGAAATGAGTTTGA 2160
 Db 2101 TGTAAAGTTTGAAAAACAGTTTATCTGTTTATTAACAGAGAAATGAGTTTGA 2160
 QY 2161 CGTCTTTTACTTGAATTTCAACTTATTAATTAAGAGAGAAAGTAAAGTGTGAAATAC 2220
 Db 2161 CGTCTTTTACTTGAATTTCAACTTATTAATTAAGAGAGAAAGTAAAGTGTGAAATAC 2220
 QY 2221 TTAACACATATCAGAAAGATGCCAAAAATGCTGAAGTTTAAACAGTGCATGTTTCCAT 2280
 Db 2221 TTAACACATATCAGAAAGATGCCAAAAATGCTGAAGTTTAAACAGTGCATGTTTCCAT 2280
 QY 2281 GCATCTTCATGATCATTAAGATGTAAGTAAAGTTTGAAGTTTAAAGTAAAGTAAAGTAA 2340
 Db 2281 GCATCTTCATGATCATTAAGATGTAAGTAAAGTTTGAAGTTTAAAGTAAAGTAAAGTAA 2340
 QY 2341 TTTTCTGTCATCAAAACAAACAGGTATCAGTGCATTAATTAATGAATTAATTAATTAATGA 2400
 Db 2341 TTTTCTGTCATCAAAACAAACAGGTATCAGTGCATTAATTAATGAATTAATTAATTAATGA 2400
 QY 2401 CATACACAGTATTTTATGTCATCTTCTTAAATTCAGACATGAATTAATTTGAATTT 2460
 Db 2401 CATACACAGTATTTTATGTCATCTTCTTAAATTCAGACATGAATTAATTTGAATTT 2460
 QY 2461 TCTAAATTCATAGGGTAGATCACCTGTAAAGCTTGTGTAATCTTAAAGTTATTAATA 2520
 Db 2461 TCTAAATTCATAGGGTAGATCACCTGTAAAGCTTGTGTAATCTTAAAGTTATTAATA 2520
 QY 2521 CTGTAACATATACCAAAAGAAAGCTGCTGTGATTTAAATCTGTAAATTCAGATGAATTT 2580
 Db 2521 CTGTAACATATACCAAAAGAAAGCTGCTGTGATTTAAATCTGTAAATTCAGATGAATTT 2580
 QY 2581 TTAACACATGCTTGTAAAAATTTTAAAGATGCTGCTTCTTCAACCAAGATTA 2640
 Db 2581 TTAACACATGCTTGTAAAAATTTTAAAGATGCTGCTTCTTCAACCAAGATTA 2640
 QY 2641 AACCTTTTAACTGTGAAGCTTTAAATCAAAATGCAAAATTTTAAAG 2700
 Db 2641 AACCTTTTAACTGTGAAGCTTTAAATCAAAATGCAAAATTTTAAAG 2700
 QY 2701 TGTGAGAGCCATGCAAGTATATCTCAAAATTAAGATATCTGTTGAGATATTCAGAAAT 2760
 Db 2701 TGTGAGAGCCATGCAAGTATATCTCAAAATTAAGATATCTGTTGAGATATTCAGAAAT 2760
 QY 2761 CTGTTTAAATGCTGCTGTAACATGTAATAACCCCAACCCGCAAAAGGGGTCTTACC 2820
 Db 2761 CTGTTTAAATGCTGCTGTAACATGTAATAACCCCAACCCGCAAAAGGGGTCTTACC 2820
 QY 2821 TTGAACATTAAGCAATTAACCAAAAGAGAAAGCCCAATTTTGTGTTCAAAATTTAGGGT 2880
 Db 2821 TTGAACATTAAGCAATTAACCAAAAGAGAAAGCCCAATTTTGTGTTCAAAATTTAGGGT 2880

QY 2881 TTAACCTTTTGAAGCAACTTTTATAGCTTGTGCACTGCAAGCTGTATCTGAT 2940
 Db 2881 TTAACCTTTTGAAGCAACTTTTATAGCTTGTGCACTGCAAGCTGTATCTGAT 2940
 QY 2941 TTTGCTATGAGGTTAAAGATGACCAAGCTGCTGTAATTAAGATATGTTTCTGAT 3000
 Db 2941 TTTGCTATGAGGTTAAAGATGACCAAGCTGCTGTAATTAAGATATGTTTCTGAT 3000
 QY 3001 TTTGCTATGAGGTTAAAGATGACCAAGCTGCTGTAATTAAGATATGTTTCTGAT 3060
 Db 3001 TTTGCTATGAGGTTAAAGATGACCAAGCTGCTGTAATTAAGATATGTTTCTGAT 3060
 QY 3061 ATAAATTAACCTCTTCAAAATGCTTAAATTCATTTCAATTTCAATTTATCTGATCTG 3120
 Db 3061 ATAAATTAACCTCTTCAAAATGCTTAAATTCATTTCAATTTCAATTTATCTGATCTG 3120
 QY 3121 AAGCAATTCAGTATGATGATGTAATCAAGCTGCTGCTGATGCTGCTGCTGCTGCTG 3180
 Db 3121 AAGCAATTCAGTATGATGATGTAATCAAGCTGCTGCTGATGCTGCTGCTGCTGCTG 3180
 QY 3181 TTTCTCTTTTATGCAATTTTGTGTAAGACACAGCTGCTGTAACATTTGTTCTGCTA 3240
 Db 3181 TTTCTCTTTTATGCAATTTTGTGTAAGACACAGCTGCTGTAACATTTGTTCTGCTA 3240
 QY 3241 TTTGTTTATGATGTTTAAAGATCAGAGTCTTCTTGTGATCTGCTGCTGCTGCTGCTG 3300
 Db 3241 TTTGTTTATGATGTTTAAAGATCAGAGTCTTCTTGTGATCTGCTGCTGCTGCTGCTG 3300
 QY 3301 TACCTGAACTTTTGCAGTTTCAAGTAAACCTGACCTGACGATGCTGATTTAGCTCTC 3360
 Db 3301 TACCTGAACTTTTGCAGTTTCAAGTAAACCTGACCTGACGATGCTGATTTAGCTCTC 3360
 QY 3361 TTAAGAAATTAATAAAAAAAAAAAG 3387
 Db 3361 TTAAGAAATTAATAAAAAAAAAAAG 3387

RESULT 5
 ABA94344
 ID ABA94344 standard; DNA, 3387 BP.
 AC ABA94344;
 XX
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human cyclooxygenase-2 (COX-2) protein encoding DNA.
 XX
 KW Cyclooxygenase; COX-1; COX-2; canine; arthritis; cancer; neoplasia;
 KW inflammation; central nervous system; human; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH CDS 98..1912
 FT Location/Qualifiers
 FT /*tag= a
 FT /transl_except= (pos: 589..591, aa: Glu)
 FT /product= "COX-1"
 EN
 XX
 PD 15-FEB-2001.
 XX
 PF 04-AUG-2000; 2000WO-US019565.
 XX
 PR 06-AUG-1999; 99US-0147601P.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PI Gliese JK;
 XX
 DR WPI; 2002-113777/15.
 DR P-PSDB; ABB07244.
 XX

Novel substantially purified canine cyclooxygenase 1 or 2 protein, useful for identifying drugs that can reduce inflammation in dogs, and screening selective inhibitors of cyclooxygenase-2 protein.

Disclosure; Page 94-97; 122pp; English.

The invention relates to genes that encode canine cyclooxygenase (COX)-1 or COX-2 proteins. The COX proteins, especially COX-2 is useful for diagnosing or prognosing a COX-2 related condition in a dog. COX-2 or its fragment is useful for identifying a test material which has the ability to inhibit, suppress, modulate, or maintain canine COX-2 activity. The COX-1 and COX-2 polynucleotides are useful for determining an association between a polymorphism and a trait. COX-2 cDNA molecules and methods provided are also useful for diagnosing or prognosing COX-2 related condition such as arthritis, cancer, neoplasia, inflammation or central nervous system disorder in a dog. The present sequence represents a human COX-2 protein encoding DNA

Sequence 3387 BP; 1010 A; 712 C; 633 G; 1032 T; 0 U; 0 Other;

Query Match 99.8%; Score 3379; DB 6; Length 3387;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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1 GTCCAGGAACCTCCTCAGCAGCGCTCTCTCAGCTCCACAGCCAGAGCCCTCAGACAGA 60
1 GTCCAGGAACCTCCTCAGCAGCGCTCTCTCAGCTCCACAGCCAGAGCCCTCAGACAGA 60
61 AAGCCTACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
61 AAGCCTACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
121 GGGCGCGGCTCTGGCGGCTCAGCCTACAGCAATCCTGCTGCTCCCAATGTCAGAA 180
121 GGGCGCGGCTCTGGCGGCTCAGCCTACAGCAATCCTGCTGCTCCCAATGTCAGAA 180
181 CGAGAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
181 CGAGAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
241 ATTCTATGAGAAACCTGCTCAACACCGGAATTTTGAACAAGATTAATTTCTGAA 300
241 ATTCTATGAGAAACCTGCTCAACACCGGAATTTTGAACAAGATTAATTTCTGAA 300
301 ACCCATCCCAACAGAGTGACATACATCTTACCCCTTCAAGGATTTTGAAGCTGT 360
301 ACCCATCCCAACAGAGTGACATACATCTTACCCCTTCAAGGATTTTGAAGCTGT 360
361 GAATAACATTCCTCTCTCTGAAATGCAATTTATGATGATGATGATGATGATGAT 420
361 GAATAACATTCCTCTCTCTGAAATGCAATTTATGATGATGATGATGATGATGAT 420
421 TTGATTTGACAGTCCACCACTTACATGCTGATGCTGATGCTGATGCTGATGCTG 480
421 TTGATTTGACAGTCCACCACTTACATGCTGATGCTGATGCTGATGCTGATGCTG 480
481 CTTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
481 CTTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
541 CTTGAGTGTCAAGAGTAAAGAGAGCTTCTCTGATTCATTAATGAGATTTGGAAAA 600
541 CTTGAGTGTCAAGAGTAAAGAGAGCTTCTCTGATTCATTAATGAGATTTGGAAAA 600
601 TCTAAGAGAAAGTTCAATCTCTCTGATCCCGAGGGCTCAAAATGATGTTTGATTT 660
601 TCTAAGAGAAAGTTCAATCTCTCTGATCCCGAGGGCTCAAAATGATGTTTGATTT 660
661 CGAGCACTTACGACAGAGTTTTCAGAGAGATCATTAAGAGAGGCGACCTTACCAA 720
661 CGAGCACTTACGACAGAGTTTTCAGAGAGATCATTAAGAGAGGCGACCTTACCAA 720
721 CGAGCTGGGCGCATGGGGTGAGCTTAATCATATTAGAGTAACTCTGCTAGACAGCG 780
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721 CGAGCTGGGCGCATGGGGTGAGCTTAATCATATTAGAGTAACTCTGCTAGACAGCG 780
781 TAAATGGGCTTTTCAAGAGTGAAGAAATGAATATCAGTAATTTGAGAGAGATGA 840
781 TAAATGGGCTTTTCAAGAGTGAAGAAATGAATATCAGTAATTTGAGAGAGATGA 840
841 TCTCTCCACAGTCAAAAGATCTCAGGAGAGATGATCCTCCTCCTCAGTCCCTGACA 900
841 TCTCTCCACAGTCAAAAGATCTCAGGAGAGATGATCCTCCTCCTCAGTCCCTGACA 900
901 TCTACGTTTCTGTGGGCGAGAGGCTTTTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 960
901 TCTACGTTTCTGTGGGCGAGAGGCTTTTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 960
961 CACATCTGGCGTGGGAGAACCAACAGAGTATGATGATGCTTAAACAGAGACCTCTGA 1020
961 CACATCTGGCGTGGGAGAACCAACAGAGTATGATGATGCTTAAACAGAGACCTCTGA 1020
1021 ATGGGATGATGAGCAGTGTCTTCCAGACAGAGCTAATCTGATGAGAGACTTATTA 1080
1021 ATGGGATGATGAGCAGTGTCTTCCAGACAGAGCTAATCTGATGAGAGACTTATTA 1080
1081 GATTGTGATGAGATTTATATGAGCAACTTGAAGGCTTATCAGCTTCAACTGAAATTTGA 1140
1081 GATTGTGATGAGATTTATATGAGCAACTTGAAGGCTTATCAGCTTCAACTGAAATTTGA 1140
1141 CCGAGACACTCTTTCAACAAACATTCAGATCCAAATGCTATGCTGCTGAAATTTAA 1200
1141 CCGAGACACTCTTTCAACAAACATTCAGATCCAAATGCTATGCTGCTGAAATTTAA 1200
1201 CACCTCTATCACTGGCATCCCTCTCTGCTGACACCTTTCAAATTCATGACCAAGATA 1260
1201 CACCTCTATCACTGGCATCCCTCTCTGCTGACACCTTTCAAATTCATGACCAAGATA 1260
1261 CAACTATCAAGTTTATTTATTAACAACCTATATGCTGGAACATGAAATTAACAGATT 1320
1261 CAACTATCAAGTTTATTTATTAACAACCTATATGCTGGAACATGAAATTAACAGATT 1320
1321 TGTGTAATCATTCACAGGCAATTTGCTGACAGGCTGTGCTGATGAGATGTTCCACC 1380
1321 TGTGTAATCATTCACAGGCAATTTGCTGACAGGCTGTGCTGATGAGATGTTCCACC 1380
1381 CGCAGTACAGAAAGTATCAAGGCTTCTTCACTGACACAGCAGCAGATGAAATTAACAG 1440
1381 CGCAGTACAGAAAGTATCAAGGCTTCTTCACTGACACAGCAGCAGATGAAATTAACAG 1440
1441 TTTTATGATGATCCGAAAGCTTTATGCTGAAGCTTATGATGATGATGATGATGAT 1500
1441 TTTTATGATGATCCGAAAGCTTTATGCTGAAGCTTATGATGATGATGATGATGAT 1500
1501 AGAGAGAAAGAAATGCTGACAGATTTGAGACATCTATGCTGATGATGATGATGAT 1560
1501 AGAGAGAAAGAAATGCTGACAGATTTGAGACATCTATGCTGATGATGATGATGAT 1560
1561 GCTGTATCTGCTCTCTCTGATGAGAAAGCTCGGCGAGATGCAATCTTTGCTGAAACCAT 1620
1561 GCTGTATCTGCTCTCTCTGATGAGAAAGCTCGGCGAGATGCAATCTTTGCTGAAACCAT 1620
1621 GGTAGAGTTTGAAGCAACATCTCTTGAAGAGCTTATGAGGATGATGATGATGAT 1680
1621 GGTAGAGTTTGAAGCAACATCTCTTGAAGAGCTTATGAGGATGATGATGATGAT 1680
1681 TGCTTACTGAGAACCAAGACATTTTGTGTGAGAGAGGTTTCAATCATCAACACTGC 1740
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1741 CTAATTCAGTCTCTCATCTGCAATTAACGTAAGAGGCTGTCCCTTAACTTCATTCAG 1800
1741 CTAATTCAGTCTCTCATCTGCAATTAACGTAAGAGGCTGTCCCTTAACTTCATTCAG 1800
1801 TCCAGATCCAGACCTCATTTAAACAGTCAACATCAATGCAAGTCTCTCCGCTCGGACT 1860
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Db 1801 TCCAGATCCAGAGCTCATTTAAACAGTCACATCAATGCAAGTTCTTCCCGCTCCGAGCT 1860
 Qy 1861 AGATGATATCATCCACAGTACTACTAAAGACGGTCGATGAACTGTAGAAAGTCTAA 1920
 Db 1861 AGATGATATCATCCACAGTACTACTAAAGACGGTCGATGAAAGTGTAGAAAGTCTAA 1920
 Qy 1921 TGATCATATTTATTTATTTATATGAAACATGTCATTTAATTTAATTAATTAATTT 1980
 Db 1921 TGATCATATTTATTTATTTATATGAAACATGTCATTTAATTTAATTAATTAATTT 1980
 Qy 1981 ATATTAAGCTCCTTATGTTACTTAACATCTTCTGTACAGAGAGTCACTCCTGTTGGG 2040
 Db 1981 ATATTAAGCTCCTTATGTTACTTAACATCTTCTGTACAGAGAGTCACTCCTGTTGGG 2040
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 Db 2041 GAGAAAGAGTCACTTGTGAAAGCTTTATGTCATCTACTCTAAGATTTTGTCTGTC 2100
 Qy 2101 TGTATAGTTTGAAGAAACAGTTTATTTATCTGTTTATTAACAGAGAGAAATGATTTGA 2160
 Db 2101 TGTATAGTTTGAAGAAACAGTTTATTTATCTGTTTATTAACAGAGAGAAATGATTTGA 2160
 Qy 2161 CGCTCTTTTACTGTAATTTCAACTATATTTATGAGAGAGAAAGTAAAGATTTGAATTC 2220
 Db 2161 CGCTCTTTTACTGTAATTTCAACTATATTTATGAGAGAGAAAGTAAAGATTTGAATTC 2220
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 Db 2221 TTAAACACTATACAAAGATGCCAAATGCTGAAAGTTTTCACATGTCGATGTTTCCAAT 2280
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 Db 2281 GGATCTTCATGATGATTTAGAAAGTACATGTTTGAATTTTAAAGTACTTTTGGGTA 2340
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 Qy 3361 TTAAGAGATTTAAAAAAG 3387
 Db 3361 TTAAGAGATTTAAAAAAG 3387
 RESULT 6
 ABZ96809
 ID ABZ96809 standard; DNA; 3387 BP.
 AC
 XX ABZ96809;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 XX Human nucleic acid sequence.
 DE
 XX
 KM Human; antisense; lung dysfunction; nasal airway dysfunction;
 KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KM antischmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
 KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KM lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PE 23-APR-2002; 2002W0-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,
 PI Miller S, Tang L, Shahbuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX

PS Disclosure, SEQ ID NO 12051; 872bp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_sequences

XX Sequence 3387 BP; 1010 A; 712 C; 633 G; 1032 T; 0 U; 0 Other;

Query Match 99.8%; Score 3379; DB 7; Length 3387;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 5; Indels 0; Gaps 0;

Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCCAGAACTCTCTGAGAGCGCCCTCTCAGCTCCAGCCAGCAGCGCCCTGAGCAGCA 60
DB 1 GTCCAGAACTCTCTGAGAGCGCCCTCTCAGCTCCAGCTCCAGCAGCGCCCTGAGCAGCA 60
QY 61 AAGCTTACCCCGCGCGCGCGCCCTGCGCGCGCTGCGATGCTGCGCGCGCCCTGCTGCT 120
DB 61 AAGCTTACCCCGCGCGCGCGCCCTGCGCGCGCTGCGATGCTGCGCGCGCCCTGCTGCT 120
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DB 121 GTGCGCGGTCTGGCGCTCAGCATACAGCAAACTCTGCTGTCCACCCATGTCATAAA 180
QY 121 GTGCGCGGTCTGGCGCTCAGCATACAGCAAACTCTGCTGTCCACCCATGTCATAAA 180
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QY 181 CCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 CCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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DB 361 GATAAATCTCCCTCTCTGAAATGCAATTAATGATGATGATGATGATGATGATGATGAT 420
QY 421 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
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QY 541 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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DB 841 TCTCTCCACAGTCAAAAGTACTCAGGACAGATGATGATGATGATGATGATGATGATGATGAT 900
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DB 901 TCTACGTTTGT 960
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 Db 3121 AAGCCAAATTCAGTATGATGCAATCAAGCTGCTGCTGATGCTGCTCTTCT 3180
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 Qy 3361 TTAAAGAGATTTAAAAAAG 3387
 Db 3361 TTAAAGAGATTTAAAAAAG 3387
 RESULT 7
 ACF63365
 ID ACF63365 standard; DNA; 3387 BP.
 XX ACF63365;
 AC
 XX
 DT 09-OCT-2003 (first entry)
 XX
 DE Human cyclooxygenase 2 gene SEQ ID NO:87.
 XX
 KW Human; pharmacological; hypotensive; antilipidemic; vasotropic; laxative;
 KW dermatological; antidepressant; tranquilizer; antiinflammatory; eczema;
 KW antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic;
 KW gynecological; virucide; vulnereary; antiarthritic; antipsoriatic; cold;
 KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;
 KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;
 KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;
 KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;
 KW constipation; headache; seizure; multiple sclerosis; polymyositis;
 KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma;
 KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;
 KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatic;
 KW inflammation; heart burn; infection; colon cancer; malignant melanoma;
 KW skin disorder; gene; ds.
 OS Homo sapiens.
 XX
 XX WO2003006478-A1.
 XX
 XX 23-JAN-2003.
 PD
 XX 10-JUL-2002; 2002WO-US021664.
 PF
 XX 10-JUL-2001; 2001US-0303820P.
 PR

QY	2581	TTATCATCATGCTGGTTTAAATATTTTATATAGAGATGCTCTTTTCCACCAAGATATA	2640		
Db	2581	TTATCAAAATGCTGGTAAAAATTTTATATAGATGCTCTTTTCCACCAAGATATA	2640		
QY	2641	AACCTTTTAGGTGATGCTTAAACCTCTCTTTAAATCAAAATGCCAAATTTATAGG	2700		
Db	2641	AACCTTTTAGGTGATGCTTAAACCTCTCTTTAAATCAAAATGCCAAATTTATAGG	2700		
QY	2701	TGGTGGAGCCACTGCAATGTTATCTCAAAATAGAAATCTCTGTGGATATTTCCAGAT	2760		
Db	2701	TGGTGGAGCCACTGCAATGTTATCTCAAAATAGAAATCTCTGTGGATATTTCCAGAT	2760		
QY	2761	CTGTTTATATGGCTGTGTAACATGTATAAAAACCCCATTAACCCGCCAAAAAGGGGTCTAACC	2820		
Db	2761	CTGTTTATATGGCTGTGTAACATGTATAAAAACCCCATTAACCCGCCAAAAAGGGGTCTAACC	2820		
QY	2821	TTGAACATTAAGCAATTAACCAAGAGAGAAAGCCCAATTAATGGTCCAAATTTAGGGT	2880		
Db	2821	TTGAACATTAAGCAATTAACCAAGAGAGAAAGCCCAATTAATGGTCCAAATTTAGGGT	2880		
QY	2881	TTAAACTTTTGAAGCAAACTTTTTTTAGCCTTGTCACATGCAAGCTGTACTAGAT	2940		
Db	2881	TTAAACTTTTGAAGCAAACTTTTTTTAGCCTTGTCACATGCAAGCTGTACTAGAT	2940		
QY	2941	TTTGCATAGAGTTAATGATATACCAAGCTGTGTTGAATAGATATGTTTCTCAGAT	3000		
Db	2941	TTTGCATAGAGTTAATGATATACCAAGCTGTGTTGAATAGATATGTTTCTCAGAT	3000		
QY	3001	TTTCTGTGTACAGTTAAATTATAGCAGTCCAAATCAATGCAAAAGTAGCAATGACATC	3060		
Db	3001	TTTCTGTGTACAGTTAAATTATAGCAGTCCAAATCAATGCAAAAGTAGCAATGACATC	3060		
QY	3061	ATAAATATACCTCTTCAAAATGCTTAAATCAATTCACATTAATTTATATTCAGCTTG	3120		
Db	3061	ATAAATATACCTCTTCAAAATGCTTAAATCAATTCACATTAATTTATATTCAGCTTG	3120		
QY	3121	AAGCAATTCAGTATGATGTCATTTGGAAATCAAGCCGGTACCTGCAAGCTGTCTCTTTCT	3180		
Db	3121	AAGCAATTCAGTATGATGTCATTTGGAAATCAAGCCGGTACCTGCAAGCTGTCTCTTTCT	3180		
QY	3181	TTTCTCTTTTAGCCATTTTGTCTAAGAGACAGTCTTCCAAACACTTCGTTCTCCTTA	3240		
Db	3181	TTTCTCTTTTAGCCATTTTGTCTAAGAGACAGTCTTCCAAACACTTCGTTCTCCTTA	3240		
QY	3241	TTTTGTTTACTAGTTTAAAGATCAAGATTCACCTTCTTTTGAATCTGCGCTATATTTTCT	3300		
Db	3241	TTTTGTTTACTAGTTTAAAGATCAAGATTCACCTTCTTTTGAATCTGCGCTATATTTTCT	3300		
QY	3301	TACCTGAATCTTTTGCAAGTTTTCAGGTAACCTCAGCTCAGACATGCTATATTTAGCTCTTC	3360		
Db	3301	TACCTGAATCTTTTGCAAGTTTTCAGGTAACCTCAGCTCAGACATGCTATATTTAGCTCTTC	3360		
QY	3361	TTAAGAAATTTAAAAAAG 3387			
Db	3361	TTAAGAAATTTAAAAAAG 3387			
RESULT 8					
ID	AAA34995	standard; DNA; 15240 BP.			
XX	AAA34995;				
XX	28-JUL-2000	(first entry)			
DE	Human adenosine receptor related polynucleotide SEQ ID NO:2684.				
XX	Human, adenosine receptor; low adenosine antisense oligonucleotide;				
KW	phosphorothioate; impaired respiration; inflammation; allergy;				
KW	allergic disease; bronchoconstriction; inhibitor; antiinflammatory;				
KW	antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;				
KW	lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;				

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
OS Homo sapiens.
XX MO200009525-A2.
XX 24-FEB-2000.
XX 03-AUG-1999; 99WO-US017712.
XX 03-AUG-1998; 98US-0095212P.
XX (UYEC-) UNIV EAST CAROLINA.
XX NYce JW;
XX WPI; 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX cancers.
XX
XX Disclosure; Page 893-897; 1343p; English.
XX
XX The present invention describes a new composition comprising an antisense
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets
XX nucleic acids involved in bronchoconstriction, allergies, and/or
XX inflammation. The ON can have antiinflammatory, antiallergic,
XX antiasthmatic, cyostatic and analgesic activities. The compositions are
XX useful for the treatment of diseases associated with inflammation,
XX impaired airways, including lung disease and diseases whose secondary
XX effects afflict the lungs of a subject. They can be used for treating
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
XX impaired respiration, respiratory distress syndrome, pain, cystic
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
XX carcinomas, and cancers which may metastasise to the lungs, including
XX breast and prostate cancer. The reduction of the adenine content of the
XX ONs reduces side effects. The A-containing ONs break down with the
XX release of deoxyadenosine which activates adenosine receptors causing
XX bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
XX nucleotide sequences given in the sequence listing from the present
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
XX sequences are also called SEQ ID NO:1 to 185, but the sequences differ
XX from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
XX AAA33992) are specifically claimed ONs from the present invention. N.B.
XX Sequences given in the disclosure of the present invention do not match
XX up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
XX
XX Sequence 15240 BP; 4672 A; 2944 C; 2804 G; 4820 T; 0 U; 0 Other;
SQ
Query Match 99.8%; Score 3379; DB 3; Length 15240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GTCCAGGAATCCTCTGAGAGCGCTCTTCAAGCTCCAGCCAGAGCGCCCTAGACAGCA 60
DB 2401 GTCCAGGAATCCTCTGAGAGCGCTCTTCAAGCTCCAGCCAGAGCGCCCTAGACAGCA 2460
QY 61 AAGCTTACCCCGCGCGCGCGCTCTGCGCGCGCTGCGAGAGCTGCGCGCGCGCTGCTGT 120
DB 2461 AAGCTTACCCCGCGCGCGCGCTCTGCGCGCGCTGCGAGAGCTGCGCGCGCGCTGCTGT 2520
QY 121 GTGCGGCGCTGCGCGCGCTGAGCCTACAGCAATCTTGTCTCCACCCATGTCAAAA 180
DB 2521 GTGCGGCGCTGCGCGCGCTGAGCCTACAGCAATCTTGTCTCCACCCATGTCAAAA 2580
QY 181 CCGAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

DB 2581 CCGAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
QY 241 ATTCTATGAGAAACCTGCTCAACCGCAATTTTGGACAAGATATAATTTATTTGAAA 300
DB 2641 ATTCTATGAGAAACCTGCTCAACCGCAATTTTGGACAAGATATAATTTATTTGAAA 2700
QY 301 ACCCACTCCAAACAGTGCATCAATCTTACCCTTCAAGGATTTTGGAACTTTGT 360
DB 2701 ACCCACTCCAAACAGTGCATCAATCTTACCCTTCAAGGATTTTGGAACTTTGT 2760
QY 361 GAATAAATTCCTCTCTTGGAAATGCAATTAAGTATGTTGTGACATCCAGATCA 420
DB 2761 GAATAAATTCCTCTCTTGGAAATGCAATTAAGTATGTTGTGACATCCAGATCA 2820
QY 421 TTTGATTGACAGTCCCAACCTTACATGCTGATGCTGATGCTGCAAAAAGCTGGAGCCT 480
DB 2821 TTTGATTGACAGTCCCAACCTTACATGCTGATGCTGATGCTGCAAAAAGCTGGAGCCT 2880
QY 481 CTCTAACCTCTCTTATTAATCTAGAGCCCTTCTCTGCTGCTGATGATTTGCCGACCTCC 540
DB 2881 CTCTAACCTCTCTTATTAATCTAGAGCCCTTCTCTGCTGCTGATGATTTGCCGACCTCC 2940
QY 541 CTTGGGTGTCAAAAGTAAAAAGCACTTCTGATTCAAATGAGATGAGAAAAATTTGCT 600
DB 2941 CTTGGGTGTCAAAAGTAAAAAGCACTTCTGATTCAAATGAGATGAGAAAAATTTGCT 3000
QY 601 TCTAAGAAAGAAAGTTCAATCCCTGATCCCAAGGCTCAAAATGATGTTGCTTTTTCG 660
DB 3001 TCTAAGAAAGAAAGTTCAATCCCTGATCCCAAGGCTCAAAATGATGTTGCTTTTTCG 3060
QY 661 CCAGACTTCACGACACCAATTTTCAAGACAGATCAATGAGGAGGCGCAGTTTTCACCA 720
DB 3061 CCAGACTTCACGACACCAATTTTCAAGACAGATCAATGAGGAGGCGCAGTTTTCACCA 3120
QY 721 CGGGCTGGCCCATGGGGGAGCTTAATCATATTTACGTTGAACTCGCTAGACACAG 780
DB 3121 CGGGCTGGCCCATGGGGGAGCTTAATCATATTTACGTTGAACTCGCTAGACACAG 3180
QY 781 TAACTGGCGCTTTTCAAGATGAGAAAAATATCATGATTAATGATGAGAGATGTA 840
DB 3181 TAACTGGCGCTTTTCAAGATGAGAAAAATATCATGATTAATGATGAGAGATGTA 3240
QY 841 TCTTCCACAGTCAAAATATCTCAGGACAGATGATCTACCTCTCTCAAGTCCCGAGCA 900
DB 3241 TCTTCCACAGTCAAAATATCTCAGGACAGATGATCTACCTCTCTCAAGTCCCGAGCA 3300
QY 901 TCTAAGTTGCTGCGGGGAGAGGCTTTGCTGCTGCTGCTGCTGATGATGATGCT 960
DB 3301 TCTAAGTTGCTGCGGGGAGAGGCTTTGCTGCTGCTGCTGCTGATGATGATGCT 3360
QY 961 CACATCTGCTGCGGGGAGACACACAGATATGATGATGATGATGATGATGATGATGAT 1020
DB 3361 CACATCTGCTGCGGGGAGACACACAGATATGATGATGATGATGATGATGATGATGAT 3420
QY 1021 ATGGGCTGATGAGAGGTTGCTTCCACACAGAGCTTAATCTGATGAGAGAGATTTAA 1080
DB 3421 ATGGGCTGATGAGAGGTTGCTTCCACACAGAGCTTAATCTGATGAGAGAGATTTAA 3480
QY 1081 GATTGATGATGAGATTAATGTCACACACTTGAAGTGGCTATCACTTCAAACTGAAATTTGA 1140
DB 3481 GATTGATGATGAGATTAATGTCACACACTTGAAGTGGCTATCACTTCAAACTGAAATTTGA 3540
QY 1141 CCGAGAACTACTTTTCAACAAATTCAGATGACCAAAATGATATTTGCTGGAATTTAA 1200
DB 3541 CCGAGAACTACTTTTCAACAAATTCAGATGACCAAAATGATATTTGCTGGAATTTAA 3600
QY 1201 CACCTCTATCACTGAGATCCCTTCTGCTGACACCTTCAAAATTCATGACAGAAATA 1260
DB 3601 CACCTCTATCACTGAGATCCCTTCTGCTGACACCTTCAAAATTCATGACAGAAATA 3660
QY 1261 CAACTATCAAGATTTATCTACAAACAATCTATATTTGCTGAAACATGGAATTAACCAAGTT 1320
DB 3661 CAACTATCAAGATTTATCTACAAACAATCTATATTTGCTGAAACATGGAATTAACCAAGTT 3720

QY	1321	TGTTGATCATTCACAGGCCAAATTTGCTG3CAGGGTGTGCTGCTGTAGAAATGTTCCACC	1380
Db	3721	TGTTGATCATTCACAGGCCAAATTTGCTG3CAGGGTGTGCTGCTGTAGAAATGTTCCACC	3780
QY	1381	CGAGATACGAAAGATATCAGAGCTTCCATTGACCAAGCAGGCGAGATGAATATCCAGTC	1440
Db	3781	CGAGATACGAAAGATATCAGAGCTTCCATTGACCAAGCAGGCGAGATGAATATCCAGTC	3840
QY	1441	TTTTAATGATACCGCAAAAGCTTTATGCTGAAGCCCTATGAATCATTTGAAAGACTTAC	1500
Db	3841	TTTTAATGATACCGCAAAAGCTTTATGCTGAAGCCCTATGAATCATTTGAAAGACTTAC	3900
QY	1501	AGAGAAAAAGAAATGCTGCGAGATTG3AAGCACTATGATGACATCATGCTGTGGA	1560
Db	3901	AGAGAAAAAGAAATGCTGCGAGATTG3AAGCACTATGATGACATCATGCTGTGGA	3960
QY	1561	GCTGATCCTGCCCCCTTCGTGTAGAAAACCTTCGCGAGATGCCATCTTTGGTGAACCAT	1620
Db	3961	GCTGATCCTGCCCCCTTCGTGTAGAAAACCTTCGCGAGATGCCATCTTTGGTGAACCAT	4020
QY	1621	GGTAGAAATGGAGACACCATTCCTCCTTGAAGAAGCTTAAGGTATGTTAATGTTCTCC	1680
Db	4021	GGTAGAAATGGAGACACCATTCCTCCTTGAAGAAGCTTAAGGTATGTTAATGTTCTCC	4080
QY	1681	TGCCATCTGGAAGCCCAAGCACTTTTGGTGAAGAGTGGGTTTCCAAATCATCAACATCGC	1740
Db	4081	TGCCATCTGGAAGCCCAAGCACTTTTGGTGAAGAGTGGGTTTCCAAATCATCAACATCGC	4140
QY	1741	CTCAATTAGTCTCTCATCTGCAATTAAGGTGAAGGGCTGTCCCTTACTTCATTCAGTGT	1800
Db	4141	CTCAATTAGTCTCTCATCTGCAATTAAGGTGAAGGGCTGTCCCTTACTTCATTCAGTGT	4200
QY	1801	TCCAGATCCAGAGCTCATTTAAACAGGTACACATGAATG3AAGTCTTCCCGCTCCGACCT	1860
Db	4201	TCCAGATCCAGAGCTCATTTAAACAGGTACACATGAATG3AAGTCTTCCCGCTCCGACCT	4260
QY	1861	AGATGATATCAATCCCAAGTACTTAATAAAGAAACGGTGCATGAACCTGTAGAAAGCTTAA	1920
Db	4261	AGATGATATCAATCCCAAGTACTTAATAAAGAAACGGTGCATGAACCTGTAGAAAGCTTAA	4320
QY	1921	TGATCATATTTATTTATTTATATGAAACCAAGTCTATTAATTTAATTTAATPATATTTT	1980
Db	4321	TGATCATATTTATTTATTTATATGAAACCAAGTCTATTAATTTAATTTAATPATATTTT	4380
QY	1981	ATATTAAACCTCTATGTTACTTAAACATCTTCGTGAACAGAGCAATCTCCTGTGTGCG	2040
Db	4381	ATATTAAACCTCTATGTTACTTAAACATCTTCGTGAACAGAGCAATCTCCTGTGTGCG	4440
QY	2041	GAGAAAGAGTCATACTTGTGAAAGACTTTTATGCACTACCTTAAGATTTGCTGTGCG	2100
Db	4441	GAGAAAGAGTCATACTTGTGAAAGACTTTTATGCACTACCTTAAGATTTGCTGTGCG	4500
QY	2101	TGTTAAGTTTGGAAAAAGTTTTTATTCGTGTTTTATTAACACAGAGAAATGATTTTGA	2160
Db	4501	TGTTAAGTTTGGAAAAAGTTTTTATTCGTGTTTTATTAACACAGAGAAATGATTTTGA	4560
QY	2161	CGTCTTTTCTTGAATTTCAACTATATATATATGAAGACGAAAGTAAAGATGTTTGAATAC	2220
Db	4561	CGTCTTTTCTTGAATTTCAACTATATATATATGAAGACGAAAGTAAAGATGTTTGAATAC	4620
QY	2221	TTTAAACATATCAACAATGCCAAAATGCTGAAGTTTTTATACCTGCGATGTTTCCAAAT	2280
Db	4621	TTTAAACATATCAACAATGCCAAAATGCTGAAGTTTTTATACCTGCGATGTTTCCAAAT	4680
QY	2281	GCATCTTCATGATGCAATTAAGAAATATATATGTTTGAATTTTAAAGTACTTTTGGGTAA	2340
Db	4681	GCATCTTCATGATGCAATTAAGAAATATATATGTTTGAATTTTAAAGTACTTTTGGGTAA	4740
QY	2341	TTTTTCGTGATCAAAAGAAACAGGTATCAGTGCATTTATTAATGAATATTTAAATTTAGA	2400
Db	4741	TTTTTCGTGATCAAAAGAAACAGGTATCAGTGCATTTATTAATGAATATTTAAATTTAGA	4800

QY	2401	CATTACACAGTAATTTTCAGTCTACACTTTTAAATGAGAAATGAAACATAATTTGCAAT	2460
Db	4801	CATTACAGTAATTTTCAGTCTACACTTTTAAATGAGAAATGAAACATAATTTGCAAT	4860
QY	2461	TCATAATTCAGGGTAGAATCACCTGTAAAAAGCTTGTGATTTCTTAAAGTAATTA	2520
Db	4861	TCATAATTCAGGGTAGAATCACCTGTAAAAAGCTTGTGATTTCTTAAAGTAATTA	4920
QY	2521	CTTGTACATATCCAAAAAGAAAGCTGTCTGGATTTAAATCTGTAAATTCAGATGA	2580
Db	4921	CTTGTACATATCCAAAAAGAAAGCTGTCTGGATTTAAATCTGTAAATTCAGATGA	4980
QY	2581	TTACTACAAATGTCTGTAAAAATTTATATAGATATGTCTTTTCACCAAGATTA	2640
Db	4981	TTACTACAAATGTCTGTAAAAATTTATATAGATATGTCTTTTCACCAAGATTA	5040
QY	2641	AACCTTTTATGTGTACCTGTAAAACTTCCTTTTAAATCAAAATGCCAAATTTAT	2700
Db	5041	AACCTTTTATGTGTACCTGTAAAACTTCCTTTTAAATCAAAATGCCAAATTTAT	5100
QY	2701	TGGTAGAGCACTGAGGTATATCCAAATATAGAAATTCCTGTGTGATATTCAGAT	2760
Db	5101	TGGTAGAGCACTGAGGTATATCCAAATATAGAAATTCCTGTGTGATATTCAGAT	5160
QY	2761	CTGTTTATATGGCTGTGTACATGTAAAAACCCATAACCCGCCAAAAAGGGGTCT	2820
Db	5161	CTGTTTATATGGCTGTGTACATGTAAAAACCCATAACCCGCCAAAAAGGGGTCT	5220
QY	2821	TTGACATATTAAGCAATATCCAAAGAGAAAAAGCCCAATATTTGGTCCAAATTT	2880
Db	5221	TTGACATATTAAGCAATATCCAAAGAGAAAAAGCCCAATATTTGGTCCAAATTT	5280
QY	2881	TTAAACTTTTGAAGCAACTTTTTTTTAGCTGTGTGACCTGTGACCTGTATCTG	2940
Db	5281	TTAAACTTTTGAAGCAACTTTTTTTTAGCTGTGTGACCTGTGACCTGTATCTG	5340
QY	2941	TTTGTATAGAGTTATATGAATGATCAAGCTGTGTGATATACATATATGTTTCT	3000
Db	5341	TTTGTATAGAGTTATATGAATGATCAAGCTGTGTGTATATGATATGTTTCT	5400
QY	3001	TTTCTGTGTACAGTTTAAATTTAGCACTCCATATCACTTTGCCAAAGTAGCAAT	3060
Db	5401	TTTCTGTGTACAGTTTAAATTTAGCACTCCATATCACTTTGCCAAAGTAGCAAT	5460
QY	3061	ATAAAAATACCTCTTCAAAATGCTTAAATTCATTTCAACATTAATTTATCTG	3120
Db	5461	ATAAAAATACCTCTTCAAAATGCTTAAATTCATTTCAACATTAATTTATCTG	5520
QY	3121	AAGCAATTCAGTAGTGTCATTTGSAATCAAGCTGTGATCTGTGATCTGTCTT	3180
Db	5521	AAGCAATTCAGTAGTGTCATTTGSAATCAAGCTGTGATCTGTGATCTGTCTT	5580
QY	3181	TTTCTCTCTTTAGCATTTTGTGATTAAGGACACAGCTCTTCCAAACAATTTG	3240
Db	5581	TTTCTCTCTTTAGCATTTTGTGATTAAGGACACAGCTCTTCCAAACAATTTG	5640
QY	3241	TTTGTGTACTAGTTTAAAGATCAGAGTCACTTTCTTTGACCTGTGCTATATTT	3300
Db	5641	TTTGTGTACTAGTTTAAAGATCAGAGTCACTTTCTTTGACCTGTGCTATATTT	5700
QY	3301	TACCTGAACCTTTTGCAAGTTTTCAGGTAAACCTCAGCTCAGAGCTGTATTT	3360
Db	5701	TACCTGAACCTTTTGCAAGTTTTCAGGTAAACCTCAGCTCAGAGCTGTATTT	5760
QY	3361	TTAAGAGATTTAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3420
Db	5761	TTAAGAGATTTAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5820
RESULT 9			
AF21117			
AF21117			
standard; DNA; 15240 BP.			

AC	AAF21117;
XX	
DT	14-MAR-2001 (first entry)

DE Human low adenosine antisense oligonucleotide related sequence #2684.

KM low adiposine antitense oligonucleotide; phosphorothiolate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoc constriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.

OS Homo sapiens.

PN WO200062736-A2.

PD 26-OCT-2000.

PF 24-MAR--2000; 2000WO-US008020.

PR 06-APR-1999; 99US-0127958P.

PA (UYEC-) UNIV EAST CAROLINA.

[illegible]

NYCE DW;
XX

DR WFL: 2000-6/95339/66.
XX

PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.

PS Disclosure; Page 968-972; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiallathmic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasocactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasocconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 15240 BP; 4672 A; 2944 C; 2804 G; 4820 T; 0 U; 0 Other;

Query Match

99.8%; Score 3379; DB 3; Length 15240;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	I	GTCCAGGAATCCTCAGACAGCGCTCTTACGTCACAGCCAGAGCGCCCTCAGACAGCA	60
Db	2401	GTCCAGGAATCCTCAGACAGCGCTCTTACGTCACAGCCAGAGCGCCCTCAGACAGCA	2460
QY	61	AAGCCTACCCCGCGCGCGCCCTGCGCGCGCGTGCGATGCTGCGCGCGCCCTGCTGT	120
Db	2461	AAGCCTACCCCGCGCGCGCCCTGCGCGCGCGTGCGATGCTGCGCGCGCCCTGCTGT	2520
QY	121	GTGCGCGGCTCTGCGCGCTCAGCCATACAGAAATCTCTGTGTCTTCCCACCCATGTCAAA	180
Db	2521	GTGCGCGGCTCTGCGCGCTCAGCCATACAGAAATCTCTGTGTCTTCCCACCCATGTCAAA	2580
QY	181	CCGAGGCTATGATATGATGTGGGATTTGACAGATAAATGCGATGTGATCCCGACAG	240
Db	2581	CCGAGGCTATGATATGATGTGGGATTTGACAGATAAATGCGATGTGATCCCGACAG	2540
QY	241	ATTCTATGAGAAATAGCTCAACCGGAATTTTGAACAGATTAATTAATTTCTGAA	300
Db	2641	ATTCTATGAGAAATAGCTCAACCGGAATTTTGAACAGATTAATTAATTTCTGAA	2700
QY	301	ACCCACTCCAAACAGACGTGACCTACATCTTACCCACTTCAAGAGATTTTGAACGTGT	360
Db	2701	ACCCACTCCAAACAGACGTGACCTACATCTTACCCACTTCAAGAGATTTTGAACGTGT	2760
QY	361	GAATACATTCCTCCTCTGAAATGCATTAATGATTAATGTGATCAGATCAGATCACA	420
Db	2761	GAATACATTCCTCCTCTGAAATGCATTAATGATTAATGTGATCAGATCAGATCACA	2820
QY	421	TTTGATTTGACGTCCACCAATTCATCAATGCTGACTATGCTTACAAAAGCTGGAAAGCTT	480
Db	2821	TTTGATTTGACGTCCACCAATTCATCAATGCTGACTATGCTTACAAAAGCTGGAAAGCTT	2880
QY	481	CTCAACCTCCCTATTTACTATAGAGCCCTCTCCCTGCTGCTGATGATAGCCGACTCC	540
Db	2881	CTCAACCTCCCTATTTACTATAGAGCCCTCTCCCTGCTGCTGATGATAGCCGACTCC	2940
QY	541	CTTGGGTGTCMAAGGTAAAAAGCAGCTTCTGATTCAAATGAGATTTGGAAAAATTGT	600
Db	2941	CTTGGGTGTCMAAGGTAAAAAGCAGCTTCTGATTCMAAGATTTGGAAAAATTGT	3000
QY	601	TCTTAGAAGAAAGTTCATCCCTGATCCCGAGGGCTCAAAATGATGTTGCATCTTTCG	660
Db	3001	TCTTAGAAGAAAGTTCATCCCTGATCCCGAGGGCTCAAAATGATGTTGTTCATCTTTCG	3060
QY	661	CCAGCACTTCACGACAGTTTTCAGAGACAGATCATACGAGGCGCAGCTTTCACCAA	720
Db	3061	CCAGCACTTCACGATCAGTTTTCAGAGACAGATCATACGAGGCGCAGCTTTCACCAA	3120
QY	721	CGGGCTGGGCGATGGGGTGAATTAAATCATATTTACGGTGAACCTGCGCTACACGCG	780
Db	3121	CGGGCTGGGCGATGGGGTGAATTAAATCATATTTACGGTGAACCTGCGCTACACGCG	3180
QY	781	TAAACTGGGCTTTTCAAGATGAGAAAAATGAATATCAGATTAATGATGAGAGATGTA	840
Db	3181	TAAACTGGGCTTTTCAAGATGAGAAAAATGAATATCAGATTAATGATGAGAGATGTA	3240
QY	841	TCTTCCACAGTCAAAAGTACTCAGCGCAGAGATGATCTACCTCTCTCAAGTCTCTGAGCA	900
Db	3241	TCTTCCACAGTCAAAAGTACTCAGCGCAGAGATGATCTACCTCTCTCAAGTCTCTGAGCA	3300
QY	901	TCTACGGTTCTGTGGGGGAGAGGCTTTGTGTGTGTGCTGCTGATGATGATGATG	960
Db	3301	TCTACGGTTCTGTGGGGGAGAGGCTTTGTGTGTGTGCTGCTGATGATGATGATG	3360
QY	961	CACAACTCGGCTGGCGGAAACAACAGAGTATGTGATGTGCTTAAACAAGACATCTTGA	1020
Db	3361	CACAACTCGGCTGGCGGAAACAACAGAGTATGTGATGTGCTTAAACAAGAGCATCTTGA	3420
QY	1021	ATGGGGTATGACAGTTGTTCCAGACAGAGGCTAATTAATGATAGAGAGCATATTA	1080

Db 3421 ATGGGGTGTAGACGCTTCTTCCAGCAACGAGCTAATATCTGATAGAGAGACTATTA 3480
 QY 1081 GATTGTGATGAAATTAATGTGCCAACACTTGAGTGGCTATCACTTCAACCTGAATTGA 1140
 Db 3481 GATTGTGATGAAATTAATGTGCCAACACTTGAGTGGCTATCACTTCAACCTGAATTGA 3540
 QY 1141 CCCAGACTACTCTTTTCAACAAACAATTCAGTACCAGAAATGCTATGCTGTGAATTAA 1200
 Db 3541 CCCAGAACTACTTTTCAACAAACAATTCAGTACCAGAAATGCTATGCTGTGAATTAA 3600
 QY 1201 CACCTCTATGACCTGGCAATCCCTCTGCTGACAGCCTTTCAAAATTCATGACCAAAATA 1260
 Db 3601 CACCTCTATGACCTGGCAATCCCTCTGCTGACAGCCTTTCAAAATTCATGACCAAAATA 3660
 QY 1261 CAACATCAACAGTTTATCTACACAACTCTATATTTGCTGGAACATGGAATTAACCAATT 1320
 Db 3661 CAACATCAACAGTTTATCTACACAACTCTATATTTGCTGGAACATGGAATTAACCAATT 3720
 QY 1321 TGTGTAATCATTTACACAGCAAAATTTGCTGGCAGGGTTGCTGGTGGTAGAAATGTTCCACC 1380
 Db 3721 TGTGTAATCATTTACACAGCAAAATTTGCTGGCAGGGTTGCTGGTGGTAGAAATGTTCCACC 3780
 QY 1381 CGCAGTACAGAAAGTATACAGGGCTTCGATGACCAAGACAGGACGATGAATTAACAGTC 1440
 Db 3781 CGCAGTACAGAAAGTATACAGGGCTTCGATGACCAAGACAGGACGATGAATTAACAGTC 3840
 QY 1441 TTTTAATGATACGCGAAACGCTTTATGCTGAAGCCCTATGAAATCATTTGAAGAATTAC 1500
 Db 3841 TTTTAATGATACGCGAAACGCTTTATGCTGAAGCCCTATGAAATCATTTGAAGAATTAC 3900
 QY 1501 AGGAGAAAGAAATGTCTGACAGTTGGAAGCACTTAATGATGATGATGATGATGATGATG 1560
 Db 3901 AGGAGAAAGAAATGTCTGACAGTTGGAAGCACTTAATGATGATGATGATGATGATGATG 3960
 QY 1561 GCTGTATCTGCTCCCTCTGATGAGAAAGCCCTGGGCAANAGCCATCTTTGGTGAACCAT 1620
 Db 3961 GCTGTATCTGCTCCCTCTGATGAGAAAGCCCTGGGCAANAGCCATCTTTGGTGAACCAT 4020
 QY 1621 GGTAGAAATGGAACACCATCTCTCTTGAAGAACTTAATGGTATGTTATATGTTCTCC 1680
 Db 4021 GGTAGAAATGGAACACCATCTCTCTTGAAGAACTTAATGGTATGTTATATGTTCTCC 4080
 QY 1681 TGCTACTGGAAGCAAGCACTTTTGGTGAAGAAAGTGGGTTTCAATCATCAACACTGC 1740
 Db 4081 TGCTACTGGAAGCAAGCACTTTTGGTGAAGAAAGTGGGTTTCAATCATCAACACTGC 4140
 QY 1741 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGCCCTTATCTTATCTCACTGT 1800
 Db 4141 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGCCCTTATCTTATCTCACTGT 4200
 QY 1801 TCCAGATCCAGAGCTCATTAACAGTCAACCATCAATGCAAGTCTTCCGCTCCGAGCT 1860
 Db 4201 TCCAGATCCAGAGCTCATTAACAGTCAACCATCAATGCAAGTCTTCCGCTCCGAGCT 4260
 QY 1861 AGATGATATCAATCCCAAGTACTTAATTAAGAAAGCGTCACTGAACCTGTAAGAGTAA 1920
 Db 4261 AGATGATATCAATCCCAAGTACTTAATTAAGAAAGCGTCACTGAACCTGTAAGAGTAA 4320
 QY 1921 TGAATCATATTTATTTATTAATGAACATGCTATTAATTTAATTTAATTAATTAATTT 1980
 Db 4321 TGAATCATATTTATTTATTAATGAACATGCTATTAATTTAATTTAATTAATTAATTT 4380
 QY 1981 ATATTAACCTCTATGTTAATTAACATCTTCTGTAACAGAACTCACTACTCTCTGCG 2040
 Db 4381 ATATTAACCTCTATGTTAATTAACATCTTCTGTAACAGAACTCACTACTCTCTGCG 4440
 QY 2041 GAGAAAGAGTCAATCTTGAAGAACTTTATGCTACTCTTAAGATTTTGGTGTGC 2100
 Db 4441 GAGAAAGAGTCAATCTTGAAGAACTTTATGCTACTCTTAAGATTTTGGTGTGC 4500
 QY 2101 TGTAAATTTGGAAGAAAGTTTTATCTGTTTATTAACAGAGAGAAATGAGTTTGA 2160
 Db 4501 TGTAAATTTGGAAGAAAGTTTTATCTGTTTATTAACAGAGAGAAATGAGTTTGA 4560

QY 2161 GCTCTTTTACTGAAATTTCACTTATATTAATGAAGAAAGTAAAGTGTGTAATAC 2220
 Db 4561 GCTCTTTTACTGAAATTTCACTTATATTAATGAAGAAAGTAAAGTGTGTAATAC 4620
 QY 2221 TTAACACTATCAAGAGATGCCAAATGCTGAAGTTTTCACGTGATGATGATGATGATG 2280
 Db 4621 TTAACACTATCAAGAGATGCCAAATGCTGAAGTTTTCACGTGATGATGATGATGATG 4680
 QY 2281 GCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
 Db 4681 GCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4740
 QY 2341 TTTTCTGCTCAACAAAGAAACAGGATCACTGATTTTAATGATATTTAATTTGA 2400
 Db 4741 TTTTCTGCTCAACAAAGAAACAGGATCACTGATTTTAATGATATTTAATTTAATTTGA 4800
 QY 2401 CATTACAGTAAATTCATGCTCACTTTTAAATAGCAATGAACATTAATTTGAATTT 2460
 Db 4801 CATTACAGTAAATTCATGCTCACTTTTAAATAGCAATGAACATTAATTTGAATTT 4860
 QY 2461 TCTAATTCATAGGGTAGAATCACTGTAAGCTTGTGATTTCTTAAAGTTAATTA 2520
 Db 4861 TCTAATTCATAGGGTAGAATCACTGTAAGCTTGTGATTTCTTAAAGTTAATTA 4920
 QY 2521 CTGTGACATTAACCAAAAGAAAGCTGCTTGGATTTAAATCTGTAATTCAGATGAAT 2580
 Db 4921 CTGTGACATTAACCAAAAGAAAGCTGCTTGGATTTAAATCTGTAATTCAGATGAAT 4980
 QY 2581 TTACTAATTCATGCTGTTAAATTTAATTAATGATGATGATGATGATGATGATGATGATG 2640
 Db 4981 TTACTAATTCATGCTGTTAAATTTAATTAATGATGATGATGATGATGATGATGATGATG 5040
 QY 2641 AACCTTTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
 Db 5041 AACCTTTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5100
 QY 2701 TGGTGAAGCACTGCAAGTGTATCTCAAAATTAAGAAATTCCTGTTGATATTTCAAGAT 2760
 Db 5101 TGGTGAAGCACTGCAAGTGTATCTCAAAATTAAGAAATTCCTGTTGATATTTCAAGAT 5160
 QY 2761 CTGTTTATGAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2820
 Db 5161 CTGTTTATGAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220
 QY 2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATTTGTTTCAATTTAAGGT 2880
 Db 5221 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATTTGTTTCAATTTAAGGT 5280
 QY 2881 TTAACCTTTTGAAGCAACCTTTTATGACCTTGTGCACTGCAAGACTGCTGATGATG 2940
 Db 5281 TTAACCTTTTGAAGCAACCTTTTATGACCTTGTGCACTGCAAGACTGCTGATGATG 5340
 QY 2941 TTGCTATGAGGTTAATGAAGTACCAAGCTGTGCTTGAATTAAGATTTTCTCGAT 3000
 Db 5341 TTGCTATGAGGTTAATGAAGTACCAAGCTGTGCTTGAATTAAGATTTTCTCGAT 5400
 QY 3001 TTTCTGTTGACGTTTAAATTTAAGAGTCCATATCACTTGCAAAAGTACATGACCTC 3060
 Db 5401 TTTCTGTTGACGTTTAAATTTAAGAGTCCATATCACTTGCAAAAGTACATGACCTC 5460
 QY 3061 ATAAATACCTCTTCAAAAGCTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTT 3120
 Db 5461 ATAAATACCTCTTCAAAAGCTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTT 5520
 QY 3121 AAGCCATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
 Db 5521 AAGCCATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5580
 QY 3181 TTTCTCTTTTACCATTTTGTGTAAGACACAGTCTTCTCAAACTTGTGTTCTCTCA 3240
 Db 5581 TTTCTCTTTTACCATTTTGTGTAAGACACAGTCTTCTCAAACTTGTGTTCTCTCA 5640

CC 3241 TTTGTTTACAGTTTAAAGTCAGAGTTCACCTTTCTTGAGCTCGCTATATTTCT 3300
 DB 5641 TTTGTTTACAGTTTAAAGTCAGAGTTCACCTTTCTTGAGCTCGCTATATTTCT 5700
 QY 3301 TACCTGAACCTTTTGCAAGTTTTCAGAGTAAACCTCAGCTCAGACTGTATTAGCTCTC 3360
 DB 5701 TACCTGAACCTTTTGCAAGTTTTCAGAGTAAACCTCAGCTCAGACTGTATTAGCTCTC 5760
 QY 3361 TTAAGAAAGTTTAAAAAAG 3387
 DB 5761 TTAAGAAAGTTTAAAAAAG 5787

RESULT 10
 ABZ96811
 ID ABZ96811 standard, DNA, 15240 BP.
 XX
 AC ABZ96811;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human nucleic acid sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasmatic; hypotensive; immunosuppressive; cytosolic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce W, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahbuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 12053; 872bp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasmatic, hypotensive,
 CC immunosuppressive, and cytosolic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 15240 BP; 4672 A; 2944 C; 2804 G; 4820 T; 0 U; 0 Other;
 SQ Query Match 99.8%; Score 3379; DB 7; Length 15240;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCCAGAACTCCCTCAGAGAGGCTCTTCAGCTCCACAGCCACAGCCCTCAGACACA 60
 DB 2401 GTCCAGAACTCCCTCAGAGAGGCTCTTCAGCTCCACAGCCACAGCCCTCAGACACA 2460
 QY 61 AAGCCTACCCCGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCT 120
 DB 2461 AAGCCTACCCCGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCT 2520
 QY 121 GTGCGCGCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 180
 DB 2521 GTGCGCGCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 2580
 QY 181 CCGAGGTGTATGTATGAGTGTGGGATTTGACAGATTAAGTGTGATCCCGGACAG 240
 DB 2581 CCGAGGTGTATGTATGAGTGTGGGATTTGACAGATTAAGTGTGATCCCGGACAG 2640
 QY 241 ATTCTATGAGAAAACTGCTCAACACCGGAAATTTTGA CAAGATTAATTTCTGAA 300
 DB 2641 ATTCTATGAGAAAACTGCTCAACACCGGAAATTTTGA CAAGATTAATTTCTGAA 2700
 QY 301 ACCCACTCCAAACACAGTGCATCATCTTACCCTTCAAGGATTTTGAAGTGT 360
 DB 2701 ACCCACTCCAAACACAGTGCATCATCTTACCCTTCAAGGATTTTGAAGTGT 2760
 QY 361 GAATTAATTCCTCTCTCTCGAAATGCAATATGATATGTTGATCATCATCATCA 420
 DB 2761 GAATTAATTCCTCTCTCTCGAAATGCAATATGATATGTTGATCATCATCATCA 2820
 QY 421 TTTGATTAACAGTCCACCACTTACATGCTGACTGATGCTTCAAAAGCTGGAAAGCTT 480
 DB 2821 TTTGATTAACAGTCCACCACTTACATGCTGACTGATGCTTCAAAAGCTGGAAAGCTT 2880
 QY 481 CTCTTAACCT 540
 DB 2881 CTCTTAACCT 2940
 QY 541 CTTGGGTGTCAAAAGTAAAGAGCTTCTGATTTCAATGATGATTTGGAATTTGCT 600
 DB 2941 CTTGGGTGTCAAAAGTAAAGAGCTTCTGATTTCAATGATGATTTGGAATTTGCT 3000
 QY 601 TCTAAGAAAGAAATTCATCTGATCTCCAGGCTCAAAATGATGTTGCAATCTTTGC 660
 DB 3001 TCTAAGAAAGAAATTCATCTGATCTCCAGGCTCAAAATGATGTTGCAATCTTTGC 3060
 QY 661 CCAGCACTTCACGACACGATTTTCAAGACAGATCATTAAGGAGGCGCAGCTTACCA 720
 DB 3061 CCAGCACTTCACGACACGATTTTCAAGACAGATCATTAAGGAGGCGCAGCTTACCA 3120
 QY 721 CGGGCTGGGCGCATGGGGTGAATTAATCATATTTACGAGTGAATCTGCTAGACAGCG 780
 DB 3121 CGGGCTGGGCGCATGGGGTGAATTAATCATATTTACGAGTGAATCTGCTAGACAGCG 3180
 QY 781 TAACTGCGCTTTCAAGAGATGAAAAATGAATATCATGATATTTGAGAGATGTA 840
 DB 3181 TAACTGCGCTTTCAAGAGATGAAAAATGAATATCATGATATTTGAGAGATGTA 3240
 QY 841 TCCCTCCACAGTCAAGTATCTCAGGACAGATGATCTTCCCTCAAGTCCCTGAGCA 900
 DB 3241 TCCCTCCACAGTCAAGTATCTCAGGACAGATGATCTTCCCTCAAGTCCCTGAGCA 3300
 QY 901 TCTAAGTGTGCTGAGGACAGAGATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 3301 TCTAAGTGTGCTGAGGACAGAGATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
 QY 961 CACAAATCTGGCTGGGAAACACACAGAGTATGTATGTCTTAAACAGGAGATCTCTA 1020

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Db 3361 CACAATCTGGCTGAGGAAACAACAAGATATGCGATGTGCTTAAACAGAGACCTCTGA 3420
Qy 1021 ATGGGGTGTATGACAGTTGTTCCAGACAAGAGGCTAATACTGATAGAGAGACTATTAA 1080
Db 3421 ATGGGGTGTATGACAGTTGTTCCAGACAAGAGGCTAATACTGATAGAGAGACTATTAA 3480
Qy 1081 GATTGTGATTGAAGATTATGTGSCAACACTTGAGTGGCTATCACTTCAAACTGAAATTGA 1140
Db 3481 GATTGTGATTGAAGATTATGTGSCAACACTTGAGTGGCTATCACTTCAAACTGAAATTGA 3540
Qy 1141 CCCGAAACACTTTTTCACAAACAATTCAGTACCAAAATGCTATTTGCTGTGAATTTAA 1200
Db 3541 CCCGAAACACTTTTTCACAAACAATTCAGTACCAAAATGCTATTTGCTGTGAATTTAA 3600
Qy 1201 CACCCTATCACTGGCAATCCCTTCTGCTGACACCTTTCAAATTCAGTACCAAAATTA 1260
Db 3601 CACCCTATCACTGGCAATCCCTTCTGCTGACACCTTTCAAATTCAGTACCAAAATTA 3660
Qy 1261 CACTATCAACAGTTTATCTACACAACCTATATTTGCTGGAACATGGAATTTACCAGTT 1320
Db 3661 CACTATCAACAGTTTATCTACACAACCTATATTTGCTGGAACATGGAATTTACCAGTT 3720
Qy 1321 TGTGAATCATTCACACAGGCAATTTGCTGGGAGGTTGCTGTGTGAAGATTTCCACC 1380
Db 3721 TGTGAATCATTCACACAGGCAATTTGCTGGGAGGTTGCTGTGTGAAGATTTCCACC 3780
Qy 1381 CGCAGTACAGAAAGTATCACAGGCTTCCATTGACAGAGACGAGAGCAATATACAGTTC 1440
Db 3781 CGCAGTACAGAAAGTATCACAGGCTTCCATTGACAGAGAGCAATATATACAGTTC 3840
Qy 1441 TTTTATATAGTACCGCAAAACGCTTATGCTGAAAGCCCTATGATCATTTTGAAGACTTAC 1500
Db 3841 TTTTATATAGTACCGCAAAACGCTTATGCTGAAAGCCCTATGATCATTTTGAAGACTTAC 3900
Qy 1501 AGGAAAGAAAGAAATGCTGAGAGTTGGAGCACTCTATGTGATCGATGCTGTGGA 1560
Db 3901 AGGAAAGAAAGAAATGCTGAGAGTTGGAGCACTCTATGTGATCGATGCTGTGGA 3960
Qy 1561 GCTGATCTGCTCCCTTCTGTAGAAAAGCTCGGCGAGATGCAATCTTTGGTGAAGACAT 1620
Db 3961 GCTGATCTGCTCCCTTCTGTAGAAAAGCTCGGCGAGATGCAATCTTTGGTGAAGACAT 4020
Qy 1621 GGTGAAGTTGAGACCACTTCTCCTTGAAAGACTTATGGGTAAATGTTATATGTTCTCC 1680
Db 4021 GGTGAAGTTGAGACCACTTCTCCTTGAAAGACTTATGGGTAAATGTTATATGTTCTCC 4080
Qy 1681 TGCCCTACGGAAGCCAAAGCACTTTTGTGAGAAAGTGGGTTTTCAAAATCATCAACACTGC 4140
Db 4081 TGCCCTACGGAAGCCAAAGCACTTTTGTGAGAAAGTGGGTTTTCAAAATCATCAACACTGC 4140
Qy 1741 CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGGGTGCTCCCTTACTTACTTCAAGT 1800
Db 4141 CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGGGTGCTCCCTTACTTACTTCAAGT 4200
Qy 4141 CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGGGTGCTCCCTTACTTACTTCAAGT 4200
Db 4141 CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGGGTGCTCCCTTACTTACTTCAAGT 4200
Qy 1801 TCCGATCCAGAGCTCATTTAAACAGTACCATCAATGCAAGTTCTTCCGCTCCGAGCT 1860
Db 4201 TCCGATCCAGAGCTCATTTAAACAGTACCATCAATGCAAGTTCTTCCGCTCCGAGCT 4260
Qy 1861 AGAGATATGATCCCAAGTACCTAATAAGAACGGTCCGACTGAACCTGTGAAGTCTAA 1920
Db 4261 AGAGATATGATCCCAAGTACCTAATAAGAACGGTCCGACTGAACCTGTGAAGTCTAA 4320
Qy 1921 TGATCATATTTATTTATTTATATGAAACATGCTATTTATTTATTTATTTATTTATTT 1980
Db 4321 TGATCATATTTATTTATTTATATGAAACATGCTATTTATTTATTTATTTATTTATTT 4380
Qy 1981 ATATTTAACTCTTATGTTACTTAAACATCTTCTGTAAACAGAGTCACTCTCTGTTCG 2040
Db 4381 ATATTTAACTCTTATGTTACTTAAACATCTTCTGTAAACAGAGTCACTCTCTGTTCG 4440
Qy 2041 GAGAAGAGTCACTACTGTGAAGACTTTTATGTCACTACTTAAAGATTTTGTGTTCG 2100
Db 4441 GAGAAGAGTCACTACTGTGAAGACTTTTATGTCACTACTTAAAGATTTTGTGTTCG 4500
Qy 2101 TGTATGTTGGAAAACAGTTTATATCTGTTTTTAAACGAGAGAAATGAGTTTTGA 2160
Db 4501 TGTATGTTGGAAAACAGTTTATATCTGTTTTTAAACGAGAGAAATGAGTTTTGA 4560
Qy 2161 CGTCTTTTACTGTAATTTCAACTAATTTATTAAGAGAAAGTAAAGTGTGGAATAC 2220
Db 4561 CGTCTTTTACTGTAATTTCAACTAATTTATTAAGAGAAAGTAAAGTGTGGAATAC 4620
Qy 2221 TTAACACTATACAAAGTCCAAATGCTGAAGTTTTCACATGTGATGTTTCCAT 2280
Db 4621 TTAACACTATACAAAGTCCAAATGCTGAAGTTTTCACATGTGATGTTTCCAT 4680
Qy 2281 GCATCTTCATGATCCATTTAAGAGTCTAATGTTTGAATTTTAAAGTACTTTGGGTA 2340
Db 4681 GCATCTTCATGATCCATTTAAGAGTCTAATGTTTGAATTTTAAAGTACTTTGGGTA 4740
Qy 2341 TTTTCTGTCATCAACAAACAAACAGGATCAGTCAATTTATTAATGAATTTAAATTTGA 2400
Db 4741 TTTTCTGTCATCAACAAACAAACAGGATCAGTCAATTTATTAATGAATTTAAATTTGA 4800
Qy 2401 CATTACAGATATTTCAATGCTACTTTTAAATCAACGAATGAACAAATTAATTTGAAT 2460
Db 4801 CATTACAGATATTTCAATGCTACTTTTAAATCAACGAATGAACAAATTAATTTGAAT 4860
Qy 2461 TCTAATTCATAGGGTGAATCACCTGTAAGCTGTGTAATTTCTTAAAGTATTTAA 2520
Db 4861 TCTAATTCATAGGGTGAATCACCTGTAAGCTGTGTAATTTCTTAAAGTATTTAA 4920
Qy 2521 CTTGATCATATACAAAGAGGCTGCTTGATTTAAATCTGTAATTCAGATGAATTT 2580
Db 4921 CTTGATCATATACAAAGAGGCTGCTTGATTTAAATCTGTAATTCAGATGAATTT 4980
Qy 2581 TTACTACATTTGCTTTTAAATTTTAAATGATGATGCTTTTTCACCAAGATTA 2640
Db 4981 TTACTACATTTGCTTTTAAATTTTAAATGATGATGCTTTTTCACCAAGATTA 5040
Qy 2641 AACCTTTTATGATGATGCTTTAAACCTCTTTAAACCAAAAGCCAAATTTATTAAG 2700
Db 5041 AACCTTTTATGATGATGCTTTAAACCTCTTTAAACCAAAAGCCAAATTTATTAAG 5100
Qy 2701 TGATGAGCCACTCAGTGTATCTCAAAATTAAGATATCTGTTGAGATTTCCAGAT 2760
Db 5101 TGATGAGCCACTCAGTGTATCTCAAAATTAAGATATCTGTTGAGATTTCCAGAT 5160
Qy 2761 CTGTTTATATGCTGTGTAACATGTAATAACCCATTAACCCCGCAAAAGGGGTCTTACC 2820
Db 5161 CTGTTTATATGCTGTGTAACATGTAATAACCCCATTAACCCCGCAAAAGGGGTCTTACC 5220
Qy 2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATGTTCCAAATTTAGGGT 2880
Db 5221 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATGTTCCAAATTTAGGGT 5280
Qy 2881 TTAACCTTTTGAAGCAACTTTTATAGCTTGTGCACTGCAAGCTGTGACTCAGAT 2940
Db 5281 TTAACCTTTTGAAGCAACTTTTATAGCTTGTGCACTGCAAGCTGTGACTCAGAT 5340
Qy 2941 TTTGCTATGAGGTTAATGAAGTACCAAGCTGTGCTTGAATGAATATGTTTCTCAGAT 3000
Db 5341 TTTGCTATGAGGTTAATGAAGTACCAAGCTGTGCTTGAATGAATATGTTTCTCAGAT 5400
Qy 3001 TTTCTGTTGTAACAGTTTAAATTTAGCAGTCAATCAATGCAAAAGGAGCAATGAGCTC 3060
Db 5401 TTTCTGTTGTAACAGTTTAAATTTAGCAGTCAATCAATGCAAAAGGAGCAATGAGCTC 5460
Qy 3061 ATAAATACCTCTTCAAAATGCTTAAATTTCAATTTCAATTTATTTATCTCAGTCTTG 3120
Db 5461 ATAAATACCTCTTCAAAATGCTTAAATTTCAATTTCAATTTATTTATCTCAGTCTTG 5520
Qy 3121 AAGCAATTCAGTATGATGCAATGGAATCAAGCTGTGCTACTGTGATGCTGTTCTTCT 3180
Db 5521 AAGCAATTCAGTATGATGCAATGGAATCAAGCTGTGCTACTGTGATGCTGTTCTTCT 5580
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Qy	3181	TTCTCTCTTTAGGCACTTTGCTGAAGAGACACAGCTCTCAAAACCTGGTTCTCTCA	3240
Dp	5881	TTTCTCTCTTTAGCCATTGTCTAAGACACAGCTCTCTAAACCTTGGTTCTCTCA	5640
Qy	3241	TTTGTGTTTACTAGTGTTTAAGTACAGAGTTCTACTTCTTTGACTCTGCTCATATTTTCT	3300
Dp	5641	TTTGTGTTTACTAGTGTTTAAGTACAGAGTTCTACTTCTTTGACTCTGCTCATATTTTCT	5700
Qy	3301	TACCTGAACCTTTTGCAGTTTTCAGGTAACTCTAGCTCAGGACTGCTATTATGACTCTC	3360
Dp	5701	TACCTGAACCTTTTGCAGTTTTCAGGTAACTCTAGCTCAGGACTGCTATTATGACTCTC	5760
Qy	3361	TTAAGAGATTTAAAAAATAAAAAAAG 3387	
Dp	5761	TTAAGAGATTTAAAAAATAAAAAAAG 5787	

RESULT 11
ABV77992

ID	ABV77992	standard; DNA; 4465 BP.
1	1	1

AC ABV779927

DT 12-NOV-2002 (first entry)

DE Hypoxia-regulated protein coding sequence #12.

KM Cyclostatic vasotropic; tranquilliser; antiathrosclerotic; gene therapy
KM antiinflammatory; vulnerrary; gynecological; ophthalmological; vaccine;
KM hypoxia; tumourigenesis; angioecrosis; apoptosis; cancer;
KM ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
KM preeclampsia; atherosclerosis; inflammatory condition; wound healing;
KM inflammation; erythropoiesis; hair loss; human; gene ds.

05 Homo sapiens.

PN W0200246465-A2.

PD 13-JUN-2002.

PF 10-DEC-2001; 2001WO-GB005458.

PR 08-DEC-2000; 2000GB-00030076.

PR 25-OCT-2001; 2001GB-00025666.

PA (OXFO-) OXFORD BIOMEDICA UK I

PI white J, Mundy CR, Ward NR, I

XX

XX

PT Identifying a gene involved in disease for treating hypoxia-regulated
 PT conditions, comprises comparing the transcriptome/proteome of two cell
 PT types under different conditions and identifying a differentially
 PT regulated gene.
 XX
 PS Claim 37, Page 339-340, 539pp; English.

CC The present invention relates to methods for identifying genes and
CC proteins that are implicated in a specific disease or physiological
CC condition. The method comprises comparing the transcriptome/proteome of a
CC specialised cell type implicated in a disease or condition with that of a
CC second specialised cell type, under two experimental conditions, and
CC identifying a gene that is differentially regulated in the two
CC specialised cell types under experimental conditions. ABV7187/ABV78116
CC and ABP65061-ABP65257 were identified using the methods of the invention.
CC The coding sequences and proteins are useful for treating a disease in a
CC patient, for manufacture of a medicament for treating hypoxia-regulated
CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
CC biological response to hypoxia conditions, or hypoxic-associated

CC pathology in a patient. The coding sequences and proteins are also useful
CC for monitoring the therapeutic treatment of a disease or physiological
CC condition, such as cancer, ischemic conditions, reperfusion injury,
CC retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory
CC conditions, wound healing, inflammation, erythropoiesis or hair loss
XX Sequence 4465 BP, 1372 A, 839 C, 813 G, 1441 T, 0 U, 0 Other;

Query Match	95.0%;	Score 3216.6;	DB 6;	Length 4465;
Best Local Similarity	97.7%;	Pred. No. 0;		
Matches 3310;	Conservative	0;	Mismatches 59;	Indels 18;
				Gaps 4;

QY	1	TTCCAGAGAACTCCCTAGAGAGGCGCTCCCTTACAGTCCACAGCCAGAGAGCGCCCTGAGACAGGA	60
Db	38	GTCCAGAGAACTCTTAGAGAGGCGCTCTTCACTCCACAGCCAGAGAGCGCCCTGAGACAGGA	97
QY	61	AAGCTTAACCCCGCGCGCGCGCTCTCCGCGCGCTGCGAGTCTCGCGCGCGCGCTGCTGCT	120
Db	98	AAGCTTAACCCCGCGCGCGCGCTCTCCGCGCGCTGCGAGTCTCGCGCGCGCGCTGCTGCT	157
QY	121	GTGCGCGGTCCTGGCGCTCAGCCATACAGCAAAATCTTGCTGTTCACCCATGTCMAAA	180
Db	158	GTGCGCGGTCCTGGCGCTCAGCCATACAGCAAAATCTTGCTGTTCACCCATGTCMAAA	217
QY	181	CCGAGGTGTATGATGAGTGTGGGATTTGACCAAGTAAAGTGCGATTTGTAACCCGACAG	240
Db	218	CCGAGGTGTATGATGAGTGTGGGATTTGACCAAGTAAAGTGCGATTTGTAACCCGACAG	277
QY	241	ATTCTATGAGAGAAACCTGCTCAACACCGGAATTTTGTGACMAAGATTTAAATTTTCTGAA	300
Db	278	ATTCTATGAGAGAAACCTGCTCAACACCGGAATTTTGTGACMAAGATTTAAATTTTCTGAA	337
QY	301	ACCCATCCAAAACAGTGCATCAATACTAACCACTTCAAGGATTTTGGAACTTGT	360
Db	338	ACCCATCCAAAACAGTGCATCAATACTAACCACTTCAAGGATTTTGGAACTTGT	397
QY	361	GAATTAACATTCCTCTCTTCGAAATGCAATTATGAGTTATGTGTGACATCCAGATCAACA	420
Db	398	GAATTAACATTCCTCTCTTCGAAATGCAATTATGAGTTATGTGTGACATCCAGATCAACA	457
QY	421	TTTGATTAACAGTCCACCACTTCAATGCTGACATGAGCTCAAAAAGCTGGAAACCTT	480
Db	458	TTTGATTAACAGTCCACCACTTCAATGCTGACATGAGCTCAAAAAGCTGGAAACCTT	517
QY	481	CTTAACTCTCTCTATTTATACTAGAGCCCTTCTCTCTGTGCTGATGATTTGCCCGACTCC	540
Db	518	CTCTAACTCTCTCTATTTATACTAGAGCCCTTCTCTCTGTGCTGATGATTTGCCCGACTCC	577
QY	541	CTTGGGTGTCAAAAGTAAAAAACAGCTTCCGTATTCATTAATGAGATTTGTGAAAAATTGT	600
Db	578	CTTGGGTGTCAAAAGTAAAAAACAGCTTCCGTATTCATTAATGAGATTTGTGAAAAATTGT	637
QY	601	TCTAAGAAAGAAATTCATCCCTGATTCGCCAGGAGCTCAAAACATGATTTTGCACTTCTTGC	660
Db	638	TCTAAGAAAGAAATTCATCCCTGATTCGCCAGGAGCTCAAAACATGATTTTGCACTTCTTGC	697
QY	661	CCAGCACTTCAAGCAACAGATTTTCAAGACAGATCATAAAGCAAGGAGCAAGCTTTCACAA	720
Db	698	CCAGCACTTCAAGCAACAGATTTTCAAGACAGATCATAAAGCAAGGAGCAAGCTTTCACAA	757
QY	721	CGGGGTGGGCCCTAGGGGTGAGCTTAAATCATATTTACGGTGAACCTCTGGCTAGACAGG	780
Db	758	CGGGGTGGGCCCTAGGGGTGAGCTTAAATCATATTTACGGTGAACCTCTGGCTAGACAGG	817
QY	781	TAAACTGCGGCTTTTCAAGAGATGAGAAAAATGAAATTCAGATTAATGATGAGAGAGATGA	840
Db	818	TAAACTGCGGCTTTTCAAGAGATGAGAAAAATGAAATTCAGATTAATGATGAGAGAGATGA	877
QY	841	TCCTCCCAAGTCAAAAGATTAATCAGGCAGAGATGATCTAACCTCTCAAGTCCCTGAGCA	900
Db	878	TCCTCCCAAGTCAAAAGATTAATCAGGCAGAGATGATCTAACCTCTCAAGTCCCTGAGCA	937
QY	901	TCCTAAGTTTGTCTGTGGGCGAGAGGCTTTTGTCTGTGGTCTGCTGTGATATGATATGC	960


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Db      938 TCTACGGTTGCTGTGCGGACAGAGGCTCTTGGTCTGCGCTGGCTGATATGTAATGC 997
Qy      961 CACAAATCGGCTGCGGGAAACACAAAGAGTATGTATGTCTTAAACAGAGCATCTGGA 1020
Db      998 CACAATCTGGCTGCGGGAAACACAAAGAGTATGTATGTCTTAAACAGAGCATCTGGA 1057
Qy     1021 ATGGGCTGATGAGCATGTTGTTCCAGACAAAGCGCTAATCTGATAGAGAGACTATTA 1080
Db     1058 ATGGGCTGATGAGCATGTTGTTCCAGACAAAGCGCTAATCTGATAGAGAGACTATTA 1117
Qy     1081 GATTGTGATGTAAGATTATGTGCAACCTTGATGGCTATGCACTTCAAACTGAATTGA 1140
Db     1118 GATTGTGATGTAAGATTATGTGCAACCTTGATGGCTATGCACTTCAAACTGAATTGA 1177
Qy     1141 CCCAGAACTACTTTTCAACAAACAAATTCAGTACCAAAATGATATGGCTGGAATTTAA 1200
Db     1178 CCCAGAACTACTTTTCAACAAACAAATTCAGTACCAAAATGATATGGCTGGAATTTAA 1237
Qy     1201 CACCCTCATCACTGGGCATTCCTCTGCTGACACCTTTCAAAATTCATGACCAAAATA 1260
Db     1238 CACCCTCATCACTGGGCATTCCTCTGCTGACACCTTTCAAAATTCATGACCAAAATA 1297
Qy     1261 CAACCTATCAAGATTATCTAACAACCTATATGTGTGAAATGTGAATTTACCAATTT 1320
Db     1298 CAACCTATCAAGATTATCTAACAACCTATATGTGTGAAATGTGAATTTACCAATTT 1357
Qy     1321 TGTGAAATCATTCACCAAGCAAAATTTGCTGAGGGTTGCTGGTGAAGATGTTCCACC 1380
Db     1358 TGTGAAATCATTCACCAAGCAAAATTTGCTGAGGGTTGCTGGTGAAGATGTTCCACC 1417
Qy     1381 CGCAGTACAGAAAGTATACAGAGCTTCATTGACCAAGACAGCAGATGAATAACAGTTC 1440
Db     1418 CGCAGTACAGAAAGTATACAGAGCTTCATTGACCAAGACAGCAGATGAATAACAGTTC 1477
Qy     1441 TTTTAATGATGACGCAAAAGCTTTATGCTGAAGCCCTTAATGATTTGAAGAACTTAC 1500
Db     1478 TTTTAATGATGACGCAAAAGCTTTATGCTGAAGCCCTTAATGATTTGAAGAACTTAC 1537
Qy     1501 AGGAGAAAAGGAAATGCTGACAGAGTTGGAAGCACTCTATGATGACATCGATGCGTGA 1560
Db     1538 AGGAGAAAAGGAAATGCTGACAGAGTTGGAAGCACTCTATGATGACATCGATGCGTGA 1597
Qy     1561 GCTGTATCTCCCTCTGCTGTAAGAAAGCCCTGCGCCAGATGCACTTTTGGTGAACCAT 1620
Db     1598 GCTGTATCTCCCTCTGCTGTAAGAAAGCCCTGCGCCAGATGCACTTTTGGTGAACCAT 1657
Qy     1621 GGTAAGATTGAGACACCATCTCCCTGAAGAAGCTTAAGGTATGTTATGTTCTCC 1680
Db     1658 GGTAAGATTGAGACACCATCTCCCTGAAGAAGCTTAAGGTATGTTATGTTCTCC 1717
Qy     1681 TGCTACTGGAAGCCAAAGCACTTTTGGTGAAGAAGTGGTTTCAAAATCATCAACATGCG 1740
Db     1718 TGCTACTGGAAGCCAAAGCACTTTTGGTGAAGAAGTGGTTTCAAAATCATCAACATGCG 1777
Qy     1741 CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGGCTGTCCCTTTAATTCAATCAGTGT 1800
Db     1778 CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGGCTGTCCCTTTAATTCAATCAGTGT 1837
Qy     1801 TCCAGATCCAGAGCTGCTTAAAGAGTCAACATTCATAGCAAGTCTTCCGCTCCGACT 1860
Db     1838 TCCAGATCCAGAGCTGCTTAAAGAGTCAACATTCATAGCAAGTCTTCCGCTCCGACT 1897
Qy     1861 AGATGATATCAATCCACAGTACTACTTAAAGAAAGCGTGCATGAACCTGTAGAAAGTAA 1920
Db     1898 AGATGATATCAATCCACAGTACTACTTAAAGAAAGCGTGCATGAACCTGTAGAAAGTAA 1957
Qy     1921 TGATCATATTTATTTATTTATATGAACCATGTCTATTAATTAATTAATTAATTAATTT 1980
Db     1958 TGATCATATTTATTTATTTATATGAACCATGTCTATTAATTAATTAATTAATTAATTT 2017
Qy     1981 ATATTAACCTCCTATGTACTTAACATCTTCTGTACAGAAAGTCACTACTCTGTGGC 2040

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Db     2018 ATATTAACCTCCTATGTACTTAACATCTTCTGTACAGAAAGTCACTACTCTGTGGC 2077
Qy     2041 GAGAAAGAGTCATCTCTGTGAAGCTTTTATGTCACTACTTAAGATTTGCTGTGC 2100
Db     2078 GAGAAAGAGTCATCTGTGAAGCTTTTATGTCACTACTTAAGATTTGCTGTGC 2137
Qy     2101 TGTTAAGTTTGAAGAAAGCTTTTATCTGTTTAAACAGAGAAATGAGTTTGA 2160
Db     2138 TGTTAAGTTTGAAGAAAGCTTTTATCTGTTTAAACAGAGAAATGAGTTTGA 2197
Qy     2161 GCTCTTTTACTTGAATTTCAACTTAATTAATTAAGAGAAAGTAAAGTGTGAATAC 2220
Db     2198 GCTCTTTTACTTGAATTTCAACTTAATTAATTAAGAGAAATGAGTTTGAATAC 2257
Qy     2221 TTAAACATATCACAAGATGCCAAATGCTGAAGTTTAACTGTGAGTGTCCAAAT 2280
Db     2258 TTAAACATATCACAAGATGCCAAATGCTGAAGTTTAACTGTGAGTGTCCAAAT 2317
Qy     2281 GCATCTTCATGATGATTAAGAGTAAATGTTGAATTTTAAAGTAACTTTGGGTA 2340
Db     2318 GCATCTTCATGATGATTAAGAGTAAATGTTGAATTTTAAAGTAACTTTGGGTA 2377
Qy     2341 TTTTCTGTCAATCAAC-AAAAAGATATCAGTGCATTTAAATGAATATTTAAATTAG 2399
Db     2378 TTTTCTGTCAATCAACAAAAAGATATCAGTGCATTTAAATGAATATTTAAATTAG 2437
Qy     2400 ACATTTACAGTAATTTCAATGCTCACTTTTAAATCAGCATGAAACAAATTTGAAT 2459
Db     2438 ACATTTACAGTAATTTCAATGCTCACTTTTAAATCAGCATGAAACAAATTTGAAT 2497
Qy     2460 TTCTAAATTCATAGGATAGAAATCACTGTAAGAGCTTTGATTTCTTAAAGTTATTA 2519
Db     2498 TTCTAAATTCATAGGATAGAAATCACTGTAAGAGCTTTGATTTCTTAAAGTTATTA 2557
Qy     2520 ACTTGATCATATACCAAAAGAGCTGTCTGGAATTAATCTGTAATCAGATGAAT 2579
Db     2558 ACTTGATCATATACCAAAAGAGCTGTCTGGAATTAATCTGTAATCAGATGAAT 2617
Qy     2580 TTACTCAATATGCTGTTTAAATATTTTATATGATGTTCTTTTACCAAGAGTAT 2639
Db     2618 TTACTCAATATGCTGTTTAAATATTTTATATGATGTTCTTTTACCAAGAGTAT 2677
Qy     2640 AAACCTTTTATAGTGTACTGTTAAACCTTCTTTAATCAAAATGCAAAATTTATTAAG 2699
Db     2678 AAACCTTTTATAGTGTACTGTTAAACCTTCTTTAATCAAAATGCAAAATTTATTAAG 2737
Qy     2700 GTGTGAGGCACTGCAAGTGTATCTCAAAATGAAGATATCTGTGAGATATTCAGAA 2759
Db     2738 GTGTGAGGCACTGCAAGTGTATCTCAAAATGAAGATATTTGTGAGATATTCAGAA 2797
Qy     2760 TCTGTTATATGCTGTGTAAATATTTTATATGATGTTCTTTTACCAAGAGTAT 2819
Db     2798 TCTGTTATATGCTGTGTAAATATTTTATATGATGTTCTTTTACCAAGAGTAT 2850
Qy     2820 CTGGAACATTAAGCAATTAACCAAGGAGAAAGCCCAATTAATGTTCCAAATTTTGGG 2879
Db     2851 TTTTAA-----AATTAAGCAATTAACCAAGGAGAAAGCCCAATTAATGTTCCAAATTTTGG 2901
Qy     2880 TTTTAACTTTTGAAGCAAACTTTTATAGCCTTGTGACCTGACAGCTGTGATCTGAGA 2939
Db     2902 GTTTAAACTTTTGAAGCAAACTTTTATAGCCTTGTGACCTGACAGCTGTGATCTGAGA 2961
Qy     2940 TTTTGTATGAGGTTTATGAAGTACCAAGCTGTGCTTGAATTAAGATATGTTTCTAGA 2999
Db     2962 TTTTGTATGAGGTTTATGAAGTACCAAGCTGTGCTTGAATTAAGATATGTTTCTAGA 3021
Qy     3000 TTTTCTGTGTACAGTTTATTTAGAGTGCATATCACTTGCAAAAGTGAATGACT 3059
Db     3022 TTTTCTGTGTACAGTTTATTTAGAGTGCATATCACTTGCAAAAGTGAATGACT 3081
Qy     3060 CATAAATACCTCTTCAAAATGCTTAAATTCATTTACACATTAATTTATCTCACTCT 3119
Db     3082 CATAAATACCTCTTCAAAATGCTTAAATTCATTTACACATTAATTTATCTCACTCT 3141

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Qy	3060	ATATAAATACCTCTTCAAAATAGCTAAATTAATTAATTCACAGCTATTTATCTCAGCTT	3112
Db	3082	CATAAATACCTCTTCAAAATAGCTAAATTAATTAATTCACAGCTATTTATCTCAGCTT	3141
Qy	3120	GAAGCCAAATTCAGTAGTGTCATTGGAAATCAAGCTGGCTACCTGCATGCTGTTCTTTTC	3179
Db	3142	GAAGCCAAATTCAGTAGTGTCATTGGAAATCAAGCTGGCTACCTGCATGCTGTTCTTTTC	3201
Qy	3180	TTTTCCTCTTTTACGCATTTTGCTATAGACACAGCTCTTCTCAAAACATTGCTTCTCCT	3239
Db	3202	TTTTCCTCTTTTACGCATTTTGCTATAGACACAGCTCTTCTC-ATCACTTGCTTCTCCT	3260
Qy	3240	ATTTTGCTTTTCTAGTTTATAGATCAGAGTTCACCTTTCTTTGGACTCTGGCTATATTTTC	3299
Db	3261	ATTTGTATTCTAGTTTATAGATCAGAGTTCACCTTTCTTTGGACTCTGGCTATATATTTTC	3320
Qy	3300	TTACCTGAACCTTTGCAGATTTTCGAGTAAACCTCAGCTCAGGACTGATATTAGTCTCCT	3359
Db	3321	TTACCTGAACCTTTGCAGATTTTCGAGTAAACCTCAGCTCAGGACTGATATTAGTCTCCT	3380
Qy	3360	CTTAAGAAAGATTTAAAAAATAAAAA 3386	
Db	3381	CTTAAGAAAGATTTAAAAAAGAAAAA 3407	

RESULT 13
 ACC57774
 ID ACC57774 standard; cDNA; 4465 BP.
 XX
 AC
 XX ACC57774;
 XX
 DT 28-JUL-2003 (first entry)
 XX
 DE Human cyclooxygenase 2 (COX-2) cDNA.
 XX
 KW Cyclooxygenase 2; COX-2; human; enzyme; vulnery; osteopathic;
 KW gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 135..1949
 FT /tag= a
 FT /product= "Human COX-2"
 XX
 EN W02003022224-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 11-SEP-2002; 2002WO-US028930.
 XX
 PR 11-SEP-2001; 2001US-00953067.
 XX
 PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 XX
 PI O'Connor PJ;
 XX
 DR WPI: 2003-313185/30.
 DR P-P8DB; ABR42250.
 XX
 PT Novel vector useful for enhancing wound healing or treating osteoporosis,
 PT osteogenesis imperfecta, and brittle bone conditions, comprises a
 PT promoter linked to a cyclooxygenase expression cassette.
 XX
 PS Disclosure; Page 66-69; 86pp; English.
 XX
 CC The present sequence is that of cDNA encoding human cyclooxygenase 2 (COX
 CC -2). A claimed vector for use in enhancing wound healing comprises a
 CC promoter linked to a COX expression cassette, especially encoding a COX-2
 CC gene product. The vector is used in claimed methods for enhancing wound
 CC healing and for enhancing wound healing following orthopaedic procedures.
 CC A claimed method for treating pathological heterotopic ossification,
 CC especially fibrodysplasia ossificans progressiva following hip

CC replacement non-steroidal antiinflammatory (NSAID) drugs. The vector is
CC also used in a claimed method for treating osteoporosis, osteogenesis
CC imperfecta and brittle bone conditions. A claimed composition for use in
CC wound healing comprises COX-1, COX-2 or both
XX
SQ Sequence 4465 BP; 1372 A; 839 C; 813 G; 1441 T; 0 U; 0 Other;

Query Match 95.0%; Score 3216.6; DB 8; Length 4465;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 3310; Conservative 0; Mismatches 59; Indels 18; Gaps 4;

QY	1	GTCCAGGAACTCTTCAGGAGGCGCTCCCTTCAAGTCCACAAGCCAGAGCGCCCTCAGACAGA	60
Db	38	GTCCAGGAACTCTTCAGGAGGCGCTCCCTTCAAGTCCACAAGCCAGAGCGCCCTCAGACAGA	97
QY	61	AAGCCTAACCCCGCGCGCGCGCTCGGCCCGCGCTCGCATGCTCGCGCGCGCCCTGCTGCT	120
Db	98	AAGCCTAACCCCGCGCGCGCGCTCGGCCCGCGCTCGCATGCTCGCGCGCGCCCTGCTGCT	157
QY	121	GTGCGCGGTCCTGGGGCTCAGGCATACAGCAAAATCCTTGCTGTTCACCCCATGTCCAAA	180
Db	158	GTGCGCGGTCCTGGGGCTCAGGCATACAGCAAAATCCTTGCTGTTCACCCCATGTCCAAA	217
QY	181	CCGAGGTATATGATAGATGTGCGATTGTGACAGATATAAGTCGATTGTATCCCGGACAG	240
Db	218	CCGAGGTATATGATAGATGTGCGATTGTGACAGATATAAGTCGATTGTATCCCGGACAG	277
QY	241	ATTCTATGGAAGAAACTGTCTCAACCGGAAATTTTGTGACMGAATPAAATTTTCTGTGA	300
Db	278	ATTCTATGGAAGAAACTGTCTCAACCGGAAATTTTGTGACMGAATPAAATTTTCTGTGA	337
QY	301	ACCACCTCCAAACACAGTGCACATACATCTTAACCCACTTCAAGGAGATTGTGACGTTGT	360
Db	338	ACCACCTCCAAACACAGTGCACATACATCTTAACCCACTTCAAGGAGATTGTGACGTTGT	397
QY	361	GAATPACATTCCTCTCTTGGAAATGCAATTATGATTATGTGTGACATCCAGATCACA	420
Db	398	GAATPACATTCCTCTCTTGGAAATGCAATTATGATTATGTCTTGCATCCAGATCACA	457
QY	421	TTTGATGTACAGTCCACCACTTAAATAGTGCATATGAGCTTCAAAAGCTGGGAAAGCCTT	480
Db	458	TTTGATGTACAGTCCACCACTTAAATAGTGCATATGAGCTTCAAAAGCTGGGAAAGCCTT	517
QY	481	CTCTAACCTCTCTATTTATCTAGAGCCCTTCTCTGTGCTGTATGTGCTCCGACCTCC	540
Db	518	CTCTAACCTCTCTATTTATCTAGAGCCCTTCTCTGTGCTGTATGTGCTCCGACCTCC	577
QY	541	CTGGGCTGCAAAAGGTAAAGACACTTCGATCCAATAGATGTGAGGAAAAATTGGT	600
Db	578	CTGGGCTGCAAAAGGTAAAGACACTTCGATCCAATAGATGTGAGGAAAAATTGGT	637
QY	601	TCTAAGAAAGAAATTCATCCCTGATCCCGAGGCTCAAAACATGATGTTTGACATCTTTG	660
Db	638	TCTAAGAAAGAAATTCATCCCTGATCCCGAGGCTCAAAACATGATGTTTGACATCTTTG	697
QY	661	CCAGACATTCACGACCAAGTTTTCAAACAGATATATAAGCAGAGGGCCAGCTTTCACCA	720
Db	698	CCAGACATTCACGACATGATTTTTCAAACAGATATATAAGCAGAGGGCCAGCTTTCACCA	757
QY	721	CGGGCTGGGGCCATGGGGTGAATTAATATCATATTTACGCTGAAACCTCTGGCTAAGACGG	780
Db	758	CGGGCTGGGGCCATGGGGTGAATTAATATCATATTTACGCTGAAACCTCTGGCTAAGACGG	817
QY	781	TAAACTGCGCCTTTTCAAGATGAGAAAAATGAATATCATCATGATTAATTGATGAGAGATGA	840
Db	818	TAAACTGCGCCTTTTCAAGATGAGAAAAATGAATATCATCATGATTAATTGATGAGAGATGA	877
QY	841	TCCCTCCACAGTCANAAGATATCTACGACAGAGATGATCTACCTCCCTCAGTCCCTGACGA	900
Db	878	TCCCTCCACAGTCANAAGATATCTACGACAGAGATGATCTACCTCCCTCAGTCCCTGACGA	937
QY	901	TCTACGGTTTGTGTGGGCGAGAGAGTCTTTGGTCTGTGCTCGGTCTGATGATGTATGC	960

Db 938 TCTACGGTTTGTCTGCGGACAGAGGCTCTTGTGCTGGTGGCTGATGATGATGAC 997
Qy 961 CACAATCTGGCTCCGGGAAACAACAAGATATGATGTGCTTAAACAGAGACTCTGA 1020
Db 998 CACAATCTGGCTCCGGGAAACAACAAGATATGCAATGTCTTAAACAGAGACTCTGA 1057
Qy 1021 ATGGGGTATGACAGCTGTCTTCAGACAAGAGGCTTAATCTGATAGAGAGACTATTAA 1080
Db 1058 ATGGGGTATGACAGCTGTCTTCAGACAAGAGGCTTAATCTGATAGAGAGACTATTAA 1117
Qy 1081 GATGTGATGATGAGATTAATGAGCACTTGAATGAGGCTATCACTTCAAACTGAAATTGA 1140
Db 1118 GATGTGATGATGAGATTAATGAGCAACCTTGAATGAGGCTATCACTTCAAACTGAAATTGA 1177
Qy 1141 CCCAGAACTACTTTTCAACAAACAATTCAGATCCAAATGATATGCTGCTGCAATTAA 1200
Db 1178 CCCAGAACTACTTTTCAACAAACAATTCAGATCCAAATGATATGCTGCTGCAATTAA 1237
Qy 1201 CACCTCTATCACTGGCACTCCCTCTGCTGCAACCTTCAAAATTCAGACCAAGAAATA 1260
Db 1238 CACCTCTATCACTGGCACTCCCTCTGCTGCAACCTTCAAAATTCAGACCAAGAAATA 1297
Qy 1261 CAACCTATCAACAGTTTATCTAACAACCTATATGCTGGAACATGGAATTACCCAGTT 1320
Db 1298 CAACCTATCAACAGTTTATCTAACAACCTATATGCTGGAACATGGAATTACCCAGTT 1357
Qy 1321 TGTGAAATCATTCACACAGCAAAATTTGCTGCAAGGCTTGTGCTGATAGAAATGTTCCACC 1380
Db 1358 TGTGAAATCATTCACACAGCAAAATTTGCTGCAAGGCTTGTGCTGATAGAAATGTTCCACC 1417
Qy 1381 CGCAGTACAGAAAGTATCAACAGGCTTCCTGATGACCAAGACAGGACAGATGAATAACAAGTC 1440
Db 1418 CGCAGTACAGAAAGTATCAACAGGCTTCCTGATGACCAAGACAGGACAGATGAATAACAAGTC 1477
Qy 1441 TTTTAAAGAGTACCGGAAAGCCTTTATGCTGAAGCCCTAATGAATCATTTGGAAGACTTAC 1500
Db 1478 TTTTAAAGAGTACCGGAAAGCCTTTATGCTGAAGCCCTAATGAATCATTTGGAAGACTTAC 1537
Qy 1501 AGGAGAAAGGAAATGTCCTGACAGATGGAAGCACTCTATGCTGACATCGATGCTGGA 1560
Db 1538 AGGAGAAAGGAAATGTCCTGACAGATGGAAGCACTCTATGCTGACATCGATGCTGGA 1597
Qy 1561 GCTGATTCCTGCCCTTCTGCTGTAAGAAAGCCTCGGACAGATCCCATCTTTGGTGAACCAT 1620
Db 1598 GCTGATTCCTGCCCTTCTGCTGTAAGAAAGCCTCGGACAGATCCCATCTTTGGTGAACCAT 1657
Qy 1621 GGTAAGAGTTGGAACACCATCTCTGCTGAAGAGCTTATGGGTAATGTTATATGTTCTCC 1680
Db 1658 GGTAAGAGTTGGAACACCATCTCTGCTGAAGAGCTTATGGGTAATGTTATATGTTCTCC 1717
Qy 1681 TGCTTACTGGAAGCAAGCACTTTTGGTGAAGAGTGGGTTTCAAAATCATCAACACTGC 1740
Db 1718 TGCTTACTGGAAGCAAGCACTTTTGGTGAAGAGTGGGTTTCAAAATCATCAACACTGC 1777
Qy 1741 CTCAATTCAGTCTCTCATCTGCAATAACGTGAAGGCTGTCCCTTTCATTCATTCAGTGT 1800
Db 1778 CTCAATTCAGTCTCTCATCTGCAATAACGTGAAGGCTGTCCCTTTCATTCATTCAGTGT 1837
Qy 1801 TCCGATCCAGAGCTGATTAATAACAGTCAACCATGAATGCAAGTTCTTCCCGCTCCGACT 1860
Db 1838 TCCGATCCAGAGCTGATTAATAACAGTCAACCATGAATGCAAGTTCTTCCCGCTCCGACT 1897
Qy 1861 AGATGATATCAATCCACAGTACTACTTAAGAAAGAGCTGCACTGAACTGTAAGAGTGA 1920
Db 1898 AGATGATATCAATCCACAGTACTACTTAAGAAAGAGCTGCACTGTAAGAGTGA 1957
Qy 1921 TGATCAATATTTATTTATTTATGAACAAGTGTATTAATTTAATTTAATTAATTT 1980
Db 1958 TGATCAATATTTATTTATTTATGAACAAGTGTATTAATTTAATTTAATTAATTT 2017
Qy 1981 ATATTAACCTCTATGTAATCTTAACATCTTCTGTAGAGAGCACTACCTCGTTGGC 2040

Db 2018 ATATTAACCTCTATGTAATCTTAACATCTTCTGTAGAGAGCACTACCTCGTTGGC 2077
Qy 2041 GAGAAAGAGTCAATCTTGTGAAGACTTTTATGCACTCACTCAAGATTTGCTGTGC 2100
Db 2078 GAGAAAGAGTCAATCTTGTGAAGACTTTTATGCACTCACTCAAGATTTGCTGTGC 2137
Qy 2101 TGTTAAGTTTGGAAACAGTTTATTTCTGTTTATTAATAACAGAGAGAAATGAGTTTGA 2160
Db 2138 TGTTAAGTTTGGAAACAGTTTATTTATCTGTTTATTAACAGAGAGAAATGAGTTTGA 2197
Qy 2161 GCTCTTTTATCTTGAATTTCACTTAATTAATAAGACGAAAGTAAAGATGTTGAATAC 2220
Db 2198 GCTCTTTTATCTTGAATTTCACTTAATTAATAAGAGTAAAGATGTTGAATAC 2257
Qy 2221 TTTAAACCTATCAAGATGCAAAATGCTGAAGTTTTCACCTGTGATGTTCCAT 2280
Db 2258 TTTAAACCTATCAAGATGCAAAATGCTGAAGTTTTCACCTGTGATGTTCCAT 2317
Qy 2281 GCATCTTCATGATGATTAAGAGTAACTAATGTTTGAATTTTAAAGTACTTTGGGTA 2340
Db 2318 GCATCTTCATGATGATTAAGAGTAACTAATGTTTGAATTTTAAAGTACTTTGGGTA 2377
Qy 2341 TTTTCTGTCACTCAAC-AAAACAGTATCACTGCAATTAATAATGAATTTAATTAAG 2399
Db 2378 TTTTCTGTCACTCAACAAAACAAACAGTATCACTGCAATTAATAATGAATTTAATTAAG 2437
Qy 2400 ACATTTACAGTAATTTCAATGCTCTTTTAAATCGCAATGGAACAATAATTGAAT 2459
Db 2438 ACATTTACAGTAATTTCAATGCTCTTTTAAATCGCAATGGAACAATAATTGAAT 2497
Qy 2460 TTTTAAATTCATAGGATAGATCACTGTAAGAAAGCTTGTGATTTCTTAAGTTATTA 2519
Db 2498 TTTTAAATTCATAGGATAGATCACTGTAAGAAAGCTTGTGATTTCTTAAGTTATTA 2557
Qy 2520 ACTTGTAATTAATCAAAAGAGCTGTCTTGATTTTAATCTGTAATCAATGAAT 2579
Db 2558 ACTTGTAATTAATCAAAAGAGCTGTCTTGATTTTAATCTGTAATCAATGAAT 2617
Qy 2580 TTTTACTCAATGCTGTTTAAATTTTAAATGATGTTTCTTTTCCAGAGAT 2639
Db 2618 TTTTACTCAATGCTGTTTAAATTTTAAATGATGTTTCTTTTCCAGAGAT 2677
Qy 2640 AAACCTTTTATGATGCTGTAAACCTCTTTTAAATCAAAATGCAAAATTTATTAAG 2699
Db 2678 AAACCTTTTATGATGCTGTAAACCTCTTTTAAATCAAAATGCAAAATTTATTAAG 2737
Qy 2700 GTGTGAGCACTGCACTGTATCTCAAAATTAAGAAATCTGTTGAGATTTCCAGAA 2759
Db 2738 GTGTGAGCACTGCACTGTATCTCAAAATTAAGAAATCTGTTGAGATTTCCAGAA 2797
Qy 2760 TCTGTTATTAATGCTGTGAATCATGTAAGAAACCCCATTAACCCCGCAAAAGGGTCTAAC 2819
Db 2798 TTTGTTATTAATGCTGTGAATCATGTAAGAAATCTATATAGC-----AAAAGGCTTAAC 2850
Qy 2820 CTGGAACATTAAGCAATTAACAAAGAGAAAGCCCAATTAATGTTCCAAATTTAGGG 2879
Db 2851 TTTTAA-----AATTAACCAATTAACAAAGAGAAACCAAAATTAATGTTCAAAATTAG 2901
Qy 2880 TTTTAACTTTTGAAGAACTTTTATGCTGTGCACTGCACTGCACTGCTGTAAGTGA 2939
Db 2902 GTTTTAACTTTTGAAGAACTTTTATGCTGTGCACTGCACTGCACTGCTGTAAGTGA 2961
Qy 2940 TTTTGTATAGGTTAATGAAGTACCAAGCTGTGTAATTAAGATATGATGTTTCTAGA 2999
Db 2962 TTTTGTATAGGTTAATGAAGTACCAAGCTGTGTAATTAAGATATGATGTTTCTAGA 3021
Qy 3000 TTTTGTGTGTACAGTTAATTTAGCACTCATATCACTTGAAGAAAGTACATGACT 3059
Db 3022 TTTTGTGTGTACAGTTAATTTAGCACTCATATCACTTGAAGAAAGTACATGACT 3081
Qy 3060 CATTAATTAATCTCTCAAAATGCTTAATTTCACTTCAACATTAATTTATCTAGCTT 3119
Db 3082 CATTAATTAATCTCTCAAAATGCTTAATTTCACTTCAACATTAATTTATCTAGCTT 3141

QY	841	TCCTCCACAGCTCAAAAGATATCTACGACAGATGATGATCTACCTCTCTCAAGTCCCTGAGCA	900
Db	878	TCCTCCACAGCTCAAAAGATATCTACGACAGATGATGATCTACCTCTCTCAAGTCCCTGAGCA	937
QY	901	TCCTACGGTTTGCTGTGGGCGAGAGGCTCTTGCTGAGGCGCTGCTGATGATGATGCG	960
Db	938	TCCTACGGTTTGCTGTGGGCGAGAGGCTCTTGCTGAGGCGCTGCTGATGATGATGCG	997
QY	961	CACAACTCGGCTGCGGGAAACAAACAGAGTATGATGATGCTTAAACAGAGCATCTCGA	1022
Db	998	CACAACTCGGCTGCGGGAAACAAACAGAGTATGATGATGCTTAAACAGAGCATCTCGA	105
QY	1021	ATGGGGGTGATGAGCAATTTGTTCCAGCAACAGCGCTAAATCTGATGAGAGACTATTAA	1086
Db	1058	ATGGGGGTGATGAGCAATTTGTTCCAGCAACAGCGCTAAATCTGATGAGAGACTATTAA	111
QY	1081	GATTTGATTTGAAGATTTATGTGCAACACTGAGTGCTATCACTTCAACCTGAATTTGA	1144
Db	1118	GATTTGATTTGAAGATTTATGTGCAACACTGAGTGCTATCACTTCAACCTGAATTTGA	1177
QY	1141	CCGAGAACTACTTTTCAACAAACAATTCCAGAACAAAATCGTATTGCGCTGAATTTAA	1200
Db	1178	CCGAGAACTACTTTTCAACAAACAANTCCAGAACAAAATCGTATTGCGCTGAATTTAA	1233
QY	1201	CACCTCTATCACTGGCATCCCTCTCTGCTGACACCTTCAATTCATGACCAAGAAATA	1260
Db	1238	CACCTCTATCACTGGCATCCCTCTCTGCTGACACCTTCAATTCATGACCAAGAAATA	1297
QY	1261	CACATCATCAAGCTTATCTACAAACAACCTATATGCTGGAAACATGGAATTAACCACTT	1328
Db	1298	CACATCATCAAGCTTATCTACAAACAACCTATATGCTGGAAACATGGAATTAACCACTT	1357
QY	1321	TGTTGAATCATTCACACAGCAAAATTGCTGACGAGGTTGCTGGTGTGAGAAATGTTCCAC	1380
Db	1358	TGTTGAATCATTCACACAGCAAAATTGCTGACGAGGTTGCTGGTGTGAGAAATGTTCCAC	1417
QY	1381	CGCAGTACAGAAAGTATACACAGGCTTCATTGACCAAGACAGGACGATGAAATACCACTC	1440
Db	1418	CGCAGTACAGAAAGTATACACAGGCTTCATTGACCAAGACAGGACGATGAAATACCACTC	1477
QY	1441	TTTTATAGATACGGCAAAACGCTTATGCTGAAGCCCTATGAAATATTTGAAGAACTTAC	1500
Db	1478	TTTTATAGATACGGCAAAACGCTTATGCTGAAGCCCTATGAAATATTTGAAGAACTTAC	1537
QY	1501	AGAGAAAAAGAAATGCTGTGACAGATTTGGAAGCACTCATGAGTGCATGCAGATGCTGGGA	1566
Db	1538	AGAGAAAAAGAAATGCTGTGACAGATTTGGAAGCACTCATGAGTGCATGCAGATGCTGGGA	1597
QY	1561	GCTGATCTCTGCCCTTCTGTGTAAGAAAGCCTCGGCAGATGCATCTTTGTGTGAACCAT	1620
Db	1598	GCTGATCTCTGCCCTTCTGTGTAAGAAAGCCTCGGCAGATGCATCTTTGTGTGAACCAT	1657
QY	1621	GGTAAATGTGGAGACCATTCCTCTTGAAGGACTTATGGGTATGTTATATGTTCTCC	1680
Db	1658	GGTAAATGTGGAGACCATTCCTCTTGAAGGACTTATGGGTATGTTATATGTTCTCC	1717
QY	1681	TGCTCACTGGAAGCAAGCACTTTTGTGTGAGAAAGTGGGCTTTCAAAATCATCAACACCTGC	1740
Db	1718	TGCTCACTGGAAGCAAGCACTTTTGTGTGAGAAAGTGGGCTTTCAAAATCATCAACACCTGC	1777
QY	1741	CTCAATTCAGTCTCTCATCTGCATTCGCAATTAACGTAAAGGCGTGTCCCTTACTTCATTCAGTGT	1800
Db	1778	CTCAATTCAGTCTCTCATCTGCATTCGCAATTAACGTAAAGGCGTGTCCCTTACTTCATTCAGTGT	1837
QY	1801	TTCCAGATCCAGAGCTCATTTAAACAGTACCATCAATGCAGAGTTCTTCCGCTCGGACT	1860
Db	1838	TTCCAGATCCAGAGCTCATTTAAACAGTACCATCAATGCAGAGTTCTTCCGCTCGGACT	1897
QY	1861	AGATGATCTCAATCCCAACAGTACTCTTAAAGAAACGGTGCAGCTGACCTGTAAAGAGCTTAA	1920
Db	1898	AGATGATCTCAATCCCAACAGTACTCTTAAAGAAACGGTGCAGCTGACCTGTAAAGAGCTTAA	1957
QY	1921	TGATCAATATTATTTATTTATGAAACCATGCTATTAAATTTAATTTAATTAATTAATTTT	1980

Db	1958	TGATCATATTATTATTTATTAATGAACCAAGCTATTAATTAATTAATTAATTAATTTT	201
QY	1981	AATATTAACCTCTTATGTACTTAACATCTTCGTGAACAGAACTGACTCCTCGTGCG	204
Db	2018	ATATTAAATCCTTTATGTACTTTAACAATCTTCGTGAACAGAACTGACTCCTCGTGCG	207
QY	2041	GAGAAAGAGTCATACTGTGTGAAGACTTTTATGTCACTACTTAAAGATTTCGTGTGC	210
Db	2078	GAGAAAGAGTCATACTGTGTGAAGACTTTTATGTCACTACTCTAAAGATTTCGTGTGC	213
QY	2101	TGTTAAGTTGGAAAAACAGTTTTCCTGTCTTTATTAACCCAGAGGAATAGCTTTTGA	216
Db	2138	TGTTAAGTTGGAAAAACAGTTTTCCTGTCTTTTAAACCCAGAGGAATAGCTTTTGA	219
QY	2161	CGTCTTTTACTGTGAATTTCAACTATATTTATGAAGCAAGATTAAGATGTTGATATC	222
Db	2198	CGTCTTTTACTGTGAATTTCAACTTATATTAATGAACAGAAAGTATGTTGATATC	225
QY	2221	TTAAACACTATACAAAGATGCCAAATGCTGAAGTTTTTACACTGTGCATGTTTCCAAAT	228
Db	2258	TTAAACACTATACAAAGATGCCAAATGCTGAAGTTTTTACACTGTGCATGTTTCCAAAT	231
QY	2281	GCATCTCCATATGATGATTAAGAAATGTTAAATGTTGAATTTTAAAGTACTTTGGGTA	234
Db	2318	GCATCTCCATATGATGATTAAGAAATGTTAAATGTTGAATTTTAAAGTACTTTGGGTA	237
QY	2341	TTTTCTGTCAATCAAC-AAAACAGTATCAGTGCATATTTAAATGAATTAATTAATTAAG	239
Db	2378	TTTTCTGTCAATCAACAAACAAAGTATCAGTGCATATTTAAATGAATTAATTAATTAAG	243
QY	2400	ACATTACAGTAATTTCAATGTCATCTTTTAAATCAGCAATGAACAAATTAATGAAT	245
Db	2438	ACATTACAGTAATTTCAATGTCATCTTTTAAATCAGCAATGAACAAATTAATGAAT	249
QY	2460	TTCTAAATTCATAGGCTAGAAATCACCTGTAAAAGCTGTGTTGATTTCTTAAAGTTATTA	251
Db	2498	TTCTAAATTCATAGGCTAGAAATCACCTGTAAAAGCTGTGTTGATTTCTTAAAGTTATTA	255
QY	2520	ACTGTACATATACCAAAAGAGCTGTCTTGATTTTAAATCGTAAATTCAGATGAAT	257
Db	2558	ACTGTACATATACCAAAAGAGCTGTCTTGATTTTAAATTCAGATGAATTCAGATGAAT	261
QY	2580	TTTACTACAAATGCTGTGTTAAATATTTTATTAAGTATGTCCTTTTCCACCAAGATAT	263
Db	2618	TTTACTACAAATGCTGTGTTAAATATTTTATTAAGTATGTCCTTTTCCACCAAGATAT	267
QY	2640	AAACCTTTTATGTGTGATCTGTAAAACCTTCTTTAAATCAAATATGCCAAATTTATTAAG	269
Db	2678	AAACCTTTTATGTGTGATCTGTAAAACCTTCTTTAAATCAAATATTTATTAAG	273
QY	2700	GTGTGTGAGCCACATCAGTGTATCTCAAAATTAAGAAATCTGTGTGAATTTCCAGAA	275
Db	2738	GTGTGTGAGCCACATCAGTGTATCTCAAAATTAAGAAATTTGTGTGAATTTCCAGAA	279
QY	2760	TCTGTTTATATGTGCTGTATAGATGTAAAACCCCATTAACCCCGCCAAAGAGGCTCTAC	281
Db	2798	TTTGTGTTTATATGTGCTGTATAGATGTAAAATCTATATCAGC-----AAAAGGCTAC	285
QY	2820	CTTGAACTAAAGCAATATACCAAGAGAGAAAAGCCCAATTAATGTGTTCCAAATTTAGGG	287
Db	2851	TTTAA-----AATTAAGCAATTAACAAAGAGAAAAGCCCAATTAATGTGTTCCAAATTTAG	290
QY	2880	TTTAACTTTTGAAGCAAACTTTTCTTAACTGTGCACTGCACTGCTGTACTCAGA	293
Db	2902	GTTTAACTTTTGAAGCAAACTTTTCTTAACTGTGCACTGCACTGCTGTACTCAGA	296
QY	2940	TTTGTCTATGAGTTAATGAAGTACCAAGCTGTGCTTGAATTAACATATGTTTCTCAGA	299
Db	2962	TTTGTCTATGAGTTAATGAAGTACCAAGCTGTGCTTGAATTAACATATGTTTCTCAGA	302
QY	3000	TTTTCTGTGTGACGTTTAATTTGCAATCATAATCAATTCAGAAAAGTACCAATGACTT	305

Db 3022 TTCTGTGTAGCATTTAATTAGCAAGTCATACATGCAAAAGTAGCAATGACCT 3081
 QY 3060 CATATAATACCTCTTCCAAAATGCTTAATTCATTTCACACATTAATTATCTAGTCTT 3119
 Db 3082 CATATAATACCTCTTCCAAAATGCTTAATTCATTTCACACATTAATTATCTAGTCTT 3141
 QY 3120 GAAGCAATTCAGTAGGTCATGGAATGCAACGCTGCTACCTGATGCTGCTCTTTC 3179
 Db 3142 GAAGCAATTCAGTAGGTCATGGAATGCAACGCTGCTACCTGATGCTGCTCTTTC 3201
 QY 3180 TTTTCTCTTTTACGCAATTTTGTCTAAGACACAGCTCTTCTCAACACTTCTGCTCT 3239
 Db 3202 TTTTCTCTTTTACGCAATTTTGTCTAAGACACAGCTCTTCTCAACACTTCTGCTCT 3260
 QY 3240 ATTTGTCTTCTGCTTTTATAGTCAGAGTCACCTTCTTGGACCTGCTATATTTTC 3299
 Db 3261 ATTTGTCTTCTGCTTTTATAGTCAGAGTCACCTTCTTGGACCTGCTATATTTTC 3320
 QY 3300 TTACCTGAACCTTTTGCAGTTTTCAGGTAAACCTCAGCTCAGACTGCTATTTAGCTCT 3359
 Db 3321 TTACCTGAACCTTTTGCAGTTTTCAGGTAAACCTCAGCTCAGACTGCTATTTAGCTCT 3380
 QY 3360 CTTAAGAAAGATTAAAAAAGAAAAA 3386
 Db 3381 CTTAAGAAAGATTAAAAAAGAAAAA 3407

RESULT 15

ACA03925 standard; cDNA; 4496 BP.

ACA03925;

27-MAY-2003 (first entry)

cDNA downregulated in senescent cells Incyte ID NO: 271804.3.

Human; senescence; ss; gene; cancer; proliferative disorder; leukemia;
 adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma;
 adrenal gland cancer; bladder cancer; bone cancer; bone marrow cancer;
 brain cancer; breast cancer; cervical cancer; colon cancer; heart cancer;
 oesophageal cancer; gall bladder cancer; ganglial cancer; kidney cancer;
 liver cancer; lung cancer; muscle cancer; ovarian cancer; penile cancer;
 pancreatic cancer; parathyroid gland cancer; prostate cancer;
 salivary gland cancer; skin cancer; small intestine cancer;
 spleen cancer; stomach cancer; testicular cancer; thymic cancer;
 thyroid cancer; uterine cancer.

Homo sapiens.

US2002192678-A1.

19-DEC-2002.

07-FEB-2002; 2002US-00071766.

09-FEB-2001; 2001US-0268380P.

(CHEN/) CHEN H.

Chen H;

WPI; 2003-328858/31.

New combination comprising cDNAs or their complements, useful for
 detecting changes in expression of genes encoding proteins associated
 with senescence, and in diagnosing, staging or treating proliferative
 diseases, e.g. cancer.

Example 13; Page 67-69; 195dp; English.

The invention relates to a combination comprising a plurality of cDNAs,
 or their complements that are differentially expressed in cancer and

other proliferative disorders. The combination is useful in detecting
 changes in expression of genes encoding proteins that are associated with
 senescence and in diagnosing, staging, treating, or monitoring the
 progression or treatment of subjects with proliferative diseases such as
 cancer e.g. adenocarcinoma, leukemia, lymphoma, melanoma, myeloma,
 sarcoma, teratocarcinoma; cancer of the adrenal gland, bladder, bone,
 bone marrow, brain, breast, cervix, colon, oesophagus, gall bladder,
 ganglia, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid
 gland, penis, prostate, salivary glands, skin, small intestine, spleen,
 stomach, testis, thymus, thyroid and uterus. The present sequence
 represents cDNA of genes that are downregulated in senescent cells

Sequence 4496 BP; 1382 A; 839 C; 816 G; 1459 T; 0 U; 0 Other;

Query Match 94.9%; Score 3215; DB 7; Length 4496;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 3309; Conservative 0; Mismatches 60; Indels 18; Gaps 4;

QY 1 GTCCAGGAATCTCTCAGAGAGGCGCTCTTCACTCCACAGCCAGCCCTCAGACAGCA 60
 Db 8 GTCCAGGAATCTCTCAGAGAGGCGCTCTTCACTCCACAGCCAGCCCTCAGACAGCA 67
 QY 61 AAGCTTACCCCGCGCGCGCGCTGCGCGCGCTGCGGATGCTGCGCGCGCGCTGCT 120
 Db 68 AAGCTTACCCCGCGCGCGCGCTGCGCGCGCTGCGGATGCTGCGCGCGCGCTGCT 127
 QY 121 GTGCGCGGCTCTGCGCGCTCAGCGCATACAGCAAACTCTTGCTCCACCCATGTCAAA 180
 Db 128 GTGCGCGGCTCTGCGCGCTCAGCGCATACAGCAAACTCTTGCTCCACCCATGTCAAA 187
 QY 181 CCGAGGTGATGATGAGTGTGGATTGACAGATTAAGTCGATTTGACCCGACAGG 240
 Db 188 CCGAGGTGATGATGAGTGTGGATTGACAGATTAAGTCGATTTGACCCGACAGG 247
 QY 241 ATTCTATGAGAAAGTCTCAACACCGGAATTTTGACAAAGATTAATATTTGCA 300
 Db 248 ATTCTATGAGAAAGTCTCAACACCGGAATTTTGACAAAGATTAATATTTGCA 307
 QY 301 ACCCACTCCAAACAGAGTCACTACATCTTACCCTCAAGGATTTTGGAAAGTTGT 360
 Db 308 ACCCACTCCAAACAGAGTCACTACATCTTACCCTCAAGGATTTTGGAAAGTTGT 367
 QY 361 GAATTAACATTCCTCTCTTGGAAATGCAATTATGATGTGTGACATCCAGATCA 420
 Db 368 GAATTAACATTCCTCTCTTGGAAATGCAATTATGATGTGTGACATCCAGATCA 427
 QY 421 TTTGATGACAGTCCACCACTTCAATGCTGACTATGCTACAAAGAGTGGAAAGCTT 480
 Db 428 TTTGATGACAGTCCACCACTTCAATGCTGACTATGCTACAAAGAGTGGAAAGCTT 487
 QY 481 CTCTAACCTCTCTATTATTAATAAGCCCTCTCTGTGCTGATGATGATGATGATGAT 540
 Db 488 CTCTAACCTCTCTATTATTAATAAGCCCTCTCTGTGCTGATGATGATGATGATGAT 547
 QY 541 CTGCGGTGTCAAAGGTAAAGACAGCTTCTGATTCAATGAGATTGGAAAAATTGCT 600
 Db 548 CTGCGGTGTCAAAGGTAAAGACAGCTTCTGATTCAATGAGATTGGAAAAATTGCT 607
 QY 601 TCTAAGAAAGAAAGTTCATCCCTGATCCCGAGGCTCAAACTGATGATGATGATGAT 660
 Db 608 TCTAAGAAAGAAAGTTCATCCCTGATCCCGAGGCTCAAACTGATGATGATGATGAT 667
 QY 661 CCAGACTTCACGACAGCAGTTTTCAGACAGATCATAGGAGGAGCCAGCTTTCACCAA 720
 Db 668 CCAGACTTCACGACAGCAGTTTTCAGACAGATCATAGGAGGAGCCAGCTTTCACCAA 727
 QY 721 CGGCGTGGGCGATGCGGCTGAGCTTAATCATATTTTACGCTGAACTCTGCTAGACAG 780
 Db 728 CGGCGTGGGCGATGCGGCTGAGCTTAATCATATTTTACGCTGAACTCTGCTAGACAG 787
 QY 781 TTAATGCGGCTTTTCAAGGATGGAAGAAATGAAATATGATTAATTTGAGAGAGATGA 840
 Db 788 TTAATGCGGCTTTTCAAGGATGGAAGAAATGAAATATGATTAATTTGAGAGAGATGA 847

QY 841 TCCTCCACAGTCAAAAGTACTCAGGCAAGATGATCTAACCTCTCAAGTCCCTGAGCA 900
DB 848 TCCTCCACAGTCAAAAGTACTCAGGCAAGATGATCTAACCTCTCAAGTCCCTGAGCA 907
QY 901 TCTAGGTTTGTGTGGGGCAGAGAGTCTTTGTCTGTGCTGGTCTGATGATGTATGC 960
DB 908 TCTAGGTTTGTGTGGGGCAGAGAGTCTTTGTCTGTGCTGGTCTGATGATGTATGC 967
QY 961 CACAATCTGGCTGCGGGGAACAACAAGAGTATGTGATGTGCTTAAAGAGAGCATCTCGA 1020
DB 968 CACAATCTGGCTGCGGGGAACAACAAGAGTATGTGATGTGCTTAAAGAGAGCATCTCGA 1027
QY 1021 ATGGGCTGATGAGCAGTGTCTTCCAGACAAGCAGGCTAATCTGATGAGAGACTATTA 1080
DB 1028 ATGGGCTGATGAGCAGTGTCTTCCAGACAAGCAGGCTAATCTGATGAGAGACTATTA 1087
QY 1081 GATTGTGATTGAAGATTATGTGCACAACCTTGAGTGGCTATCATCTTCAAACTGMAATTGGA 1140
DB 1088 GATTGTGATTGAAGATTATGTGCACAACCTTGAGTGGCTATCATCTTCAAACTGMAATTGGA 1147
QY 1141 CCCAGAACTACTTTTCAACAACAATTCAGTACCAGAAATGCTATGCTGCTGAATTAA 1200
DB 1148 CCCAGAACTACTTTTCAACAACAATTCAGTACCAGAAATGCTATGCTGCTGAATTAA 1207
QY 1201 CACCTCTATCATCTGGCAATCCCTTCTGCTGACACCTTTCAAACTGACAGAAATA 1260
DB 1208 CACCTCTATCATCTGGCAATCCCTTCTGCTGACACCTTTCAAACTGACAGAAATA 1267
QY 1261 CAACATCAACAGTATTATCTACCAACATCTATATGTGTGAAACAATGATCCAGTT 1320
DB 1268 CAACATCAACAGTATTATCTACCAACATCTATATGTGTGAAACAATGATCCAGTT 1327
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DB 1328 TGTGAAATCATCTACCGAGCAAAATTGCTGCGAGGCTTGTGCTGCTGAAGATGTTCAAC 1387
QY 1381 CGCAGTACAGAAAGTATCAAGGCTTCATTGACCAAGACAGCAGATGMAATACAGTC 1440
DB 1388 CGCAGTACAGAAAGTATCAAGGCTTCATTGACCAAGACAGCAGATGMAATACAGTC 1447
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DB 1448 TTTTAAATGATGACCGGCAAAAGCTTTATGCTGAAGACCTTATGATCATTTGAGAACTTAC 1507
QY 1501 AGGAGAAAGGAAATGTCTGCAGAGTGAAGACACTCTATGCTGACATCGATGCTGGA 1560
DB 1508 AGGAGAAAGGAAATGTCTGCAGAGTGAAGACACTCTATGCTGACATCGATGCTGGA 1567
QY 1561 GCTGTATCTGCTCTGTGTGTAAGAAAGCTCGGCAAGATGCCATCTTTGGTGAACCAT 1620
DB 1568 GCTGTATCTGCTCTGTGTGTAAGAAAGCTCGGCAAGATGCCATCTTTGGTGAACCAT 1627
QY 1621 GGTAGAGTGGGAGACCAATTCCTCTGAAAGACTTATGGGATATGTATATGTTCTGC 1680
DB 1628 GGTAGAGTGGGAGACCAATTCCTCTGAAAGACTTATGGGATATGTATATGTTCTGC 1687
QY 1681 TGGCTACTGGAAGCAAGCACTTTTGTGAGAAAGTGGGTTTTCAAATCATCAACAATGC 1740
DB 1688 TGGCTACTGGAAGCAAGCACTTTTGTGAGAAAGTGGGTTTTCAAATCATCAACAATGC 1747
QY 1741 CTGAATTCAGTCTCTCATCTGCAATAAGTGAAGGGCTGTCCCTTTAATTCTTCAATGATG 1800
DB 1748 CTGAATTCAGTCTCTCATCTGCAATAAGTGAAGGGCTGTCCCTTTAATTCTTCAATGATG 1807
QY 1801 TCCAGATCCAGAGCTCAATTAACAAGTCAACATCAATGCAAGTTCCTCCGCTCCGACT 1860
DB 1808 TCCAGATCCAGAGCTCAATTAACAAGTCAACATCAATGCAAGTTCCTCCGCTCCGACT 1867
QY 1861 AGATGATATCAATCCACAGTACTACTTAAGAAAGAGCGTGCAGTGAAGTGAAGTCTAA 1920
DB 1868 AGATGATATCAATCCACAGTACTACTTAAGAAAGAGCGTGCAGTGAAGTGAAGTCTAA 1927

QY 1921 TGATCATATTTATTTATTTATATGAAACCATGCTATTAATTAATTAATTAATTAATTT 1980
DB 1928 TGATCATATTTATTTATTTATATGAAACCATGCTATTAATTAATTAATTAATTAATTT 1987
QY 1981 AATATTAACCTCCTTATGTTACTTAAACATCTTCTGTAAACAGAGTCACTGCTGGCG 2040
DB 1988 AATATTAACCTCCTTATGTTACTTAAACATCTTCTGTAAACAGAGTCACTGCTGGCG 2047
QY 2041 GAGAAAGAGTCAATCTTGTGAAGACTTTATGTCACTACTGTAAAGATTTTGTCTGTGC 2100
DB 2048 GAGAAAGAGTCAATCTTGTGAAGACTTTATGTCACTACTGTAAAGATTTTGTCTGTGC 2107
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DB 2108 TGTAAAGTTTGAAGAAACAGTTTATCTGTTTATTAATTAACAGAGAAATGAGTTTGA 2167
QY 2161 CGTCTTTTAACTTGAATTTCAACTTAATTAATTAAGACGAAGTAAAGTGTGAATAC 2220
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DB 2228 TTAACACATCAACAAGTGCAGAAATGCTGAAGTTTATCACTGCTGATGTTCCAT 2287
QY 2281 GCATCTTCATGATGATGAAAGTAACTAATGTTTGAATTTAAAGTACTTTGGGTA 2340
DB 2288 GCATCTTCATGATGATGAAAGTAACTAATGTTTGAATTTAAAGTACTTTGGGTA 2347
QY 2341 TTTTCTGTCAATCAAC-AAAAAGTATCAAGTGCATTAATTAATGATATTTAAATTG 2399
DB 2348 TTTTCTGTCAATCAACAAAGAGTATCAAGTGCATTAATTAATGATATTTAAATTG 2407
QY 2400 ACATTTACAGTAATTTATGATGCTATCTTTTAAATCAAGATGMAATATTTGAAT 2459
DB 2408 ACATTTACAGTAATTTATGATGCTATCTTTTAAATCAAGATGMAATATTTGAAT 2467
QY 2460 TTCTAAATCATAGGGTAGAATCACTGTAAAGCTTGTGATTTCTTAAAGTATTA 2519
DB 2468 TTCTAAATCATAGGGTAGAATCACTGTAAAGCTTGTGATTTCTTAAAGTATTA 2527
QY 2520 ACTTGTACATATACCAAAAAGAGCTGTGGAATTTAAATCTGTAAATCAGATGAAT 2579
DB 2528 ACTTGTACATATACCAAAAAGAGCTGTGGAATTTAAATCTGTAAATCAGATGAAT 2587
QY 2580 TTTACTACATATGCTGTTTAAATATTTATTAAGTATGTTCTTTTACCAAGATAT 2639
DB 2588 TTTACTACATATGCTGTTTAAATATTTATTAAGTATGTTCTTTTACCAAGATAT 2647
QY 2640 AAACCTTTTAGTGTGACTGTAAACCTTCTTTAATCAAAAAGCAATTAATTAAG 2699
DB 2648 AAACCTTTTAGTGTGACTGTAAACCTTCTTTAATCAAAAAGCAATTAATTAAG 2707
QY 2700 GTGTGAGGCACTGCAAGTGTATCTCAAAATAGAAATATCTGTGAGATTTCCAGAA 2759
DB 2708 GTGTGAGGCACTGCAAGTGTATCTTAAATAGAAATATTTGTGAGATTTCCAGAA 2767
QY 2760 TCTGTTATATGCTGTGTAACATGTAAAAACCCATPACCCGCCCAAAAGGGTCTTACC 2819
DB 2768 TCTGTTATATGCTGTGTAACATGTAAAAACCTATATCAGTATGAGTATGAGTATGAG 2820
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DB 2821 TTTTAA-----AATPAGCAATTAACAAAGAAAGAAACCAATTAATTTGTTCAATTTAG 2871
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DB 2872 GTTTAACTTTTGAAGCAAACTTTTTTTATCTTGTGACCTGCAAGCCTGGTACTGAGA 2931
QY 2940 TTTTGTATGAGGTTATATGAGTACCAAGTGTGCTTGAATTAAGTATGTTTCTCAGA 2999
DB 2932 TTTTGTATGAGGTTATATGAGTACCAAGTGTGCTTGAATTAAGTATGTTTCTCAGA 2991
QY 3000 TTTTGTGTGTACAGTTTATTTATTTAGAGTCCATATACATGTCMAAAGTAGCAATGACCT 3059

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Db 2992 |T|T|T|C|T|G|T|G|A|G|C|T|T|A|A|T|T|T|G|C|A|G|T|C|A|T|A|T|C|A|T|T|G|C|A|A|A|A|G|T|A|G|C|A|A|T|G|A|C|T| 3051
Qy 3060 |C|A|T|A|A|A|T|A|C|C|T|T|T|C|A|A|A|A|T|G|C|T|T|A|A|T|T|C|A|T|T|T|C|A|C|A|T|T|A|T|T|T|A|T|C|A|G|T|C|T| 3119
Db 3052 |C|A|T|A|A|A|T|A|C|C|T|T|T|C|A|A|A|A|T|G|C|T|T|A|A|T|T|C|A|C|A|T|T|A|T|T|T|A|T|T|C|A|G|T|C|T| 3111
Qy 3120 |G|A|G|C|C|A|A|T|T|C|A|G|T|A|G|T|G|C|A|T|T|G|A|T|C|A|A|G|C|C|T|G|G|C|T|A|C|T|G|C|A|G|T|G|C|T|T|T|C| 3179
Db 3112 |G|A|G|C|C|A|A|T|T|C|A|G|T|A|G|T|G|C|A|T|T|G|A|T|C|A|A|G|C|C|T|G|G|C|T|A|C|T|G|C|A|G|T|G|C|T|T|T|C| 3171
Qy 3180 |T|T|T|C|T|T|C|T|T|T|T|A|G|C|A|T|T|T|T|G|C|T|A|G|A|C|A|C|A|G|T|T|T|C|C|A|A|A|C|A|C|T|T|G|T|T|C|C|T| 3239
Db 3172 |T|T|T|C|T|T|C|T|T|T|T|A|G|C|A|T|T|T|T|G|C|T|A|G|A|C|A|C|A|G|T|T|T|C|C|A|A|A|C|A|C|T|T|G|T|T|C|C|T| 3230
Qy 3240 |A|T|T|T|G|T|T|T|T|A|G|T|T|T|T|A|G|A|T|C|A|G|T|T|C|T|T|T|G|A|C|T|G|C|C|T|A|T|A|T|T|T|C| 3299
Db 3231 |A|T|T|T|G|T|T|T|T|A|G|T|T|T|T|T|A|G|A|T|C|A|G|T|T|C|T|T|T|G|A|C|T|G|C|C|T|A|T|A|T|T|T|C| 3290
Qy 3300 |T|T|A|C|T|G|A|C|T|T|T|G|C|A|G|T|T|T|T|C|A|G|T|T|A|A|C|T|C|A|G|C|T|G|A|C|T|G|C|T|A|T|T|A|G|C|T|C|T| 3359
Db 3291 |T|T|A|C|T|G|A|C|T|T|T|G|C|A|G|T|T|T|T|T|C|A|G|T|T|A|A|C|T|C|A|G|C|T|G|A|C|T|G|C|T|A|T|T|A|G|C|T|C|T| 3350
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Search completed: April 24, 2004, 07:47:37
Job time : 1231 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: April 24, 2004, 07:25:46 ; Search time 223 Seconds
(without alignments)
8428,783 Million cell updates/sec

Title: US-08-064-271-11

Perfect score: 3387

Sequence: 1 GTCCAGGAACTCTCAGCAG.....GATTAAAAAAAAAAAAAAAAAG 3387

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3387	100.0	3387	1	US-08-064-271-11
2	3379	99.8	3387	4	US-09-023-655-1050
3	3375.8	99.7	3387	2	US-08-627-254C-29
4	3374.2	99.6	3387	3	US-08-930-589A-19
5	3374.2	99.6	3387	4	US-09-599-781-19
6	1803.2	53.2	1834	1	US-08-487-753-3
7	1803.2	53.2	1834	1	US-08-487-753-3
8	1803.2	53.2	1834	2	US-08-480-065-3
9	1803.2	53.2	1834	2	US-08-480-065-3
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34	422.6	12.5	542	4	US-09-919-060-3	Sequence 3, Appl
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37	315.8	9.3	429	4	US-09-641-638-330	Sequence 330, Appl
38	243	7.2	243	3	US-09-437-457-2	Sequence 327, Appl
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44	132.8	3.9	602	4	US-09-702-705-1564	Sequence 1564, Ap
45	132.8	3.9	602	4	US-09-736-457-1564	Sequence 1564, Ap

ALIGNMENTS

RESULT 1
US-08-064-271-11
; Sequence 11, Application US/08064271

; Patent No. 5543297

; GENERAL INFORMATION:

APPLICANT: Kennedy, Brian P.

APPLICANT: Cromlish, Wanda A.

APPLICANT: Mancini, Joseph A.

APPLICANT: O'Neill, Gary

APPLICANT: Vickers, Philip J.

APPLICANT: Wong, Elizabeth

TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 cDNA AND

NUMBER OF SEQUENCES: 14

TITLE OF INVENTION: ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY

CORRESPONDENCE ADDRESS:

ADDRESS: Merck & Co., Inc.

STREET: 126 Lincoln Avenue

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 in, 1.4kb

COMPUTER: Apple Macintosh

OPERATING SYSTEM: System 7

SOFTWARE: Microsoft Word 5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/064,271

FILING DATE: 19930506

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Panzer, Curtis C.

REGISTRATION NUMBER: 33,752

REFERENCE/DOCKET NUMBER: 189061A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908)594-3199

TELEFAX: (908)594-4720

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 3387 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-064-271-11

Query Match 100.0%; Score 3387; DB 1; Length 3387;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3387; Conservative 0; Mismatches 0; Gaps 0;

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Dp	3241	TTTTGTGTTACTATTTTAAAGATACAGAGTTCACCTTCTTGAATCTGAGCTATATTTTCT	3300

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Db	3301	TACCTGAACCTTTTCAGAGTTTCAGGTAACCTAGCTCAGACGTGCATTATAGTCTCTC	3360
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Db	3361	TTAAGACATTTAAAAAATAAAAAAAG	3387

RESULT 2
US-09-023-655-1050

; Sequence 1050, Application US/090236555
; Patent No. 6607879

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer

```
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; NUMBER OF DRAWINGS: 10
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ADDRESSEE: INCITE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: BAY ALTO

STATE: CALIFORNIA
COUNTRY: USA

COMPTON PERDAB
ZIP: 94304

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/ COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for

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CURRENT APPLICATION DATA:
APPLICATION NUMBER:  HS/09/023 655

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FILING DATE: HEREWITH
CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

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FILING DATE: .
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1050:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3387 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single

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TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: GENBA
CLONE: g181253

US-09-023-655-1050

Query Match	99.8%;	Score 3379;	DB 4;	Length 3387;
Best Local Similarity	99.98%;	Pred. No. 0;		

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Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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D0
61

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[illegible][illegible]

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QY 481 CTCTAACCTCTCTATTTACTAGAGCCCTTCTCTGTGCTGTGATGTGCCGACATCC 540
Db 481 CTCTAACCTCTCTATTTACTAGAGCCCTTCTCTGTGCTGTGATGTGCCGACATCC 540
QY 541 CTGGGGTGTCAAAAGTAAAGACAGCTTCTGATTTCAATGAGATTTGGAAAAATTTGCT 600
Db 541 CTGGGGTGTCAAAAGTAAAGACAGCTTCTGATTTCAATGAGATTTGGAAAAATTTGCT 600
QY 601 TCTAAGAAAGAAAGTTCATCCCTGATCCCAAGGGCTCAAAACATGATGTTGGCATTTTGC 660
Db 601 TCTAAGAAAGAAAGTTCATCCCTGATCCCAAGGGCTCAAAACATGATGTTGGCATTTTGC 660
QY 661 CCAAGCACTTCCAGCACAGATTTTCAAGACAGATCATAGAGGAGGAGGAGCTTTCAACCA 720
Db 661 CCAAGCACTTCCAGCACAGATTTTCAAGACAGATCATAGAGGAGGAGGAGCTTTCAACCA 720
QY 721 CGGGGCTGGGGCCATGGGGGTGAGCTTAAATCATATTTTACGGTGAACCTTGGCTAGACAGG 780
Db 721 CGGGGCTGGGGCCATGGGGGTGAGCTTAAATCATATTTTACGGTGAACCTTGGCTAGACAGG 780
QY 781 TAAACGTGGCTTTTCAAGAGATGAGAAAATATATCATATATGATATGATGAGAGATGTA 840
Db 781 TAAACGTGGCTTTTCAAGAGATGAGAAAATATATCATATATGATATGATGAGAGATGTA 840
QY 841 TCCCTCCACAGTCAAGATATCTCAGGACAGATGATCTACCTCTCAAGTCCCTGAGCA 900
Db 841 TCCCTCCACAGTCAAGATATCTCAGGACAGATGATCTACCTCTCAAGTCCCTGAGCA 900
QY 901 TCTACGTTTGTGTGGGGCAGAGAGGCTTGTGCTGGGCTGGTGTGATGATGATGTC 960
Db 901 TCTACGTTTGTGTGGGGCAGAGAGGCTTGTGCTGGGCTGGTGTGATGATGATGTC 960
QY 961 CACAAATCTGGCTCGGGGAAACACAACAGAGTATGTGATGCTTAAACAGAGACATCTGA 1020
Db 961 CACAAATCTGGCTCGGGGAAACACAACAGAGTATGTGATGCTTAAACAGAGACATCTGA 1020
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Db 1021 ATGGGGTGTGAGCAGTGTCTCAGACAAAGAGGCTAATATGATAGGAGACATATTTAA 1080
QY 1081 GATTGTGATGAGAAATTATGTGCAACACTGATGGCTATCACTTCAAACTGAATTTTGA 1140
Db 1081 GATTGTGATGAGAAATTATGTGCAACACTGATGGCTATCACTTCAAACTGAATTTTGA 1140
QY 1141 CCCAGAACTACTTTTCAACAAACAATTCAGATACCAAAATGATATGCTGTGAATTTAA 1200
Db 1141 CCCAGAACTACTTTTCAACAAACAATTCAGATACCAAAATGATATGCTGTGAATTTAA 1200
QY 1201 CACCTCTATACCTGGCATCCCTTCTGCTGTGACACCTTTGAAATTCATGATCAGAGAAATA 1260
Db 1201 CACCTCTATACCTGGCATCCCTTCTGCTGTGACACCTTTGAAATTCATGATCAGAGAAATA 1260

QY 1261 CAACATATCAAGATTTATCTTACAAACAATCTATATTTGCTGGACATGGAATTTACCCAGTT 1320
Db 1261 CAACATATCAAGATTTATCTTACAAACAATCTATATTTGCTGGACATGGAATTTACCCAGTT 1320
QY 1321 TGTGAAATCAATTCACAGGCAAAATTTGCTGCAAGGTTTGTCTGGTGTAGGAAATGTTCCACC 1380
Db 1321 TGTGAAATCAATTCACAGGCAAAATTTGCTGCAAGGTTTGTCTGGTGTAGGAAATGTTCCACC 1380
QY 1381 CGCAGTACAGAAAGTATACAGGCTTCCATTGACACAGGAGGACAGATGAATATACAGTTC 1440
Db 1381 CGCAGTACAGAAAGTATACAGGCTTCCATTGACACAGGAGGACAGATGAATATACAGTTC 1440
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Db 1501 AGAGAAAAAGAAATGTCTGACAGATGGAAGCACTCTATGATGACATGATGCTGTGGA 1560
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Db 1621 GGTGAAAGTTGGAGACCATCTCTCTTGAAGAGCTTATGAGTATGTTATATGTTCTCC 1680
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Db 1681 TGCCCTACTGGAAGCCCAAGCACTTTTGTGTGAGAAAGTGGGTTTTCAAATCATCAACATGTC 1740
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Db 1741 CTCAATTCAGTCTCTCATCTGCAATAAGTGAAGGCTGCTCCCTTACCTGATAGTGT 1800
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Db 1801 TCCAGATCCAGAGCTCATTTAAACAGTCAACATCAATCAAGTTCTTCCCGCTCCGAGCT 1860
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Db 1861 AGATGATATCAATCCACAGTATCTATTAAGAAAGGCTGCACTGAACGTGAGAACTCTAA 1920
QY 1921 TGATCATATTTATTTATTTATATGAAACCATGCTATTAATTTATTTAATAATATTT 1980
Db 1921 TGATCATATTTATTTATTTATATGAAACCATGCTATTAATTTATTTAATAATATTT 1980
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Db 2221 TTAAACACTATATCAAGATGCAAAATGCTGAAAGTTTATACATGTCATGTTTCCAT 2280
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Db 2281 GCATCTTCATGATGATTAAGTAACTAATGTTTGAATTTTAAAGTACTTTTGGGTA 2340

QY 2341 TTTTCTGTCATCAAAACAAACAGGATATAGTCATATTAAATGAATTTAAATTAGA 2400
 Db 2341 TTTTCTGTCATCAAAACAAACAGGATATAGTCATATTAAATGAATTTAAATTAGA 2400
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 QY 2461 TCTAAATTCATAGGGTAGAATCACTGTAAAGCTGTGTAATTTCTTAAAGTTATTA 2520
 Db 2461 TCTAAATTCATAGGGTAGAATCACTGTAAAGCTGTGTAATTTCTTAAAGTTATTA 2520
 QY 2521 CTGTGACATATACCAAAAAAGAGCTGTCTGTGATTTAAATCTGTAAATCAGATGAAT 2580
 Db 2521 CTGTGACATATACCAAAAAAGAGCTGTCTGTGATTTAAATCTGTAAATCAGATGAAT 2580
 QY 2581 TTACATCAATTCCTGTTTAAATATTTTAATGATGATTTCTTTTCCAAAGATATA 2640
 Db 2581 TTACATCAATTCCTGTTTAAATATTTTAATGATGATTTCTTTTCCAAAGATATA 2640
 QY 2641 AACCTTTAGTGTGCTGTAAACTTCTTTTAAATCAAAATGCAAAATTTATTTAAG 2700
 Db 2641 AACCTTTAGTGTGCTGTAAACTTCTTTTAAATCAAAATGCAAAATTTATTTAAG 2700
 QY 2701 TGTGTGAGCACTGTGATGTTATCTCAAAATAGAAATATCTGTTGAGATATTCAGAT 2760
 Db 2701 TGTGTGAGCACTGTGATGTTATCTCAAAATAGAAATATCTGTTGAGATATTCAGAT 2760
 QY 2761 CTGTTATATGCTGTGTAATGTAATTAATCCCAATACCCCGCAAAAGGGTCTTACC 2820
 Db 2761 CTGTTATATGCTGTGTAATGTAATTAATCCCAATACCCCGCAAAAGGGTCTTACC 2820
 QY 2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTTATGTTCCAAATTTAGGT 2880
 Db 2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTTATGTTCCAAATTTAGGT 2880
 QY 2881 TTTAACTTTTGAAGCAACTTTTCTTTAGCTTGTGCACTGCAAGCTGTGACTGAT 2940
 Db 2881 TTTAACTTTTGAAGCAACTTTTCTTTAGCTTGTGCACTGCAAGCTGTGACTGAT 2940
 QY 2941 TTTGCTATGAGTGTATGAAAGTACCAAGCTGTGCTGTAATACGATATCTTTCAGAT 3000
 Db 2941 TTTGCTATGAGTGTATGAAAGTACCAAGCTGTGCTGTAATACGATATCTTTCAGAT 3000
 QY 3001 TTTCTGTGTACAGTTAATTTAGCAGTCATATCAATTTGCAAAAGTAGCAATGACCTC 3060
 Db 3001 TTTCTGTGTACAGTTAATTTAGCAGTCATATCAATTTGCAAAAGTAGCAATGACCTC 3060
 QY 3061 ATTAATAATCTCTTCAAAATGCTTAATTCATTTGACACATTTAATTTATCTCAGTCTG 3120
 Db 3061 ATTAATAATCTCTTCAAAATGCTTAATTCATTTGACACATTTAATTTATCTCAGTCTG 3120
 QY 3121 AAGCAATTCAGTAGTGATGTGAAATCAAGCTGTGCTACGTCATGCTGTCTCTTTCT 3180
 Db 3121 AAGCAATTCAGTAGTGATGTGAAATCAAGCTGTGCTACGTCATGCTGTCTCTTTCT 3180
 QY 3181 TTTCTCTTTTAAAGCAATTTGCTAAGAGACAGAGCTTCTCAAAACATTCGTTCTCTCA 3240
 Db 3181 TTTCTCTTTTAAAGCAATTTGCTAAGAGACAGAGCTTCTCAAAACATTCGTTCTCTCA 3240
 QY 3241 TTTTGTATTACAGTTTAAAGATCAGAGTTCATTTCTTTGAGCTCTGCTATATTTCT 3300
 Db 3241 TTTTGTATTACAGTTTAAAGATCAGAGTTCATTTCTTTGAGCTCTGCTATATTTCT 3300
 QY 3301 TACCTGAAGTGTGAGAGTTTCAAGTAAACCTGAGCTCAGAGATTTAGATCTCTC 3360
 Db 3301 TACCTGAAGTGTGAGAGTTTCAAGTAAACCTGAGCTCAGAGATTTAGATCTCTC 3360
 QY 3361 TTAAAGAGATTAATAAAAAAAAAAAG 3387
 Db 3361 TTAAAGAGATTAATAAAAAAAAAAAG 3387

RESULT 3
 US-08-627-254C-29
 ; Sequence 25, Application US/08627254C
 ; Patent No. 5859229
 ; GENERAL INFORMATION:
 ; APPLICANT: Knise, Douglas A.
 ; TITLE OF INVENTION: Elcosanoid Formation
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Calfee, Halter & Griwold LLP
 ; STREET: 800 Superior Avenue
 ; CITY: Cleveland
 ; STATE: Ohio
 ; COUNTRY: USA
 ; ZIP: 44114
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/627,254C
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Golrick, Mary E
 ; REGISTRATION NUMBER: 34,829
 ; REFERENCE/DOCKET NUMBER: 18525/00107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (216) 622-8200
 ; TELEFAX: (216) 241-0816
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3387 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-627-254C-29
 Query Match 99.7%; Score 3375.8; DB 2; Length 3387;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 3380; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 GTCCAGAACTCTTAGAGAGGCGCTCTTCACTTCAACAGCCAGACGCCCTTACAGACAGA 60
 Db 1 GTCCAGAACTCTTAGAGAGGCGCTCTTCACTTCAACAGCCAGACGCCCTTACAGACAGA 60
 QY 61 AAGCTTACCCCGCGCGCGCGCGCTGCGCGCGCTGCGATGCTGCGCGCGCGCTGCTGCT 120
 Db 61 AAGCTTACCCCGCGCGCGCGCGCTGCGCGCGCTGCGATGCTGCGCGCGCGCTGCTGCT 120
 QY 121 GTGCGCGGCTCTGCGCGCTAGCGCATACAGCAATCTTGTCTTCCACCCATGTCAAAA 180
 Db 121 GTGCGCGGCTCTGCGCGCTAGCGCATACAGCAATCTTGTCTTCCACCCATGTCAAAA 180
 QY 121 GTGCGCGGCTCTGCGCGCTAGCGCATACAGCAATCTTGTCTTCCACCCATGTCAAAA 180
 Db 121 GTGCGCGGCTCTGCGCGCTAGCGCATACAGCAATCTTGTCTTCCACCCATGTCAAAA 180
 QY 181 CCGAGGTGTATGATGATGTGAGATTTGACCAAGTAAAGTGGCATTTGATCCCGGACAGG 240
 Db 181 CCGAGGTGTATGATGATGTGAGATTTGACCAAGTAAAGTGGCATTTGATCCCGGACAGG 240
 QY 181 CCGAGGTGTATGATGATGTGAGATTTGACCAAGTAAAGTGGCATTTGATCCCGGACAGG 240
 Db 181 CCGAGGTGTATGATGATGTGAGATTTGACCAAGTAAAGTGGCATTTGATCCCGGACAGG 240
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 Db 241 ATTCTATGAGAGAACTGTCTCAACACCGGAATTTTGTGACAGAAATTAATTTCTGAA 300
 QY 301 ACCCACTCCAAACAGATGACTACATACCACTTCAAGGATTTTGGACGTTGT 360
 Db 301 ACCCACTCCAAACAGATGACTACATACCACTTCAAGGATTTTGGACGTTGT 360
 QY 361 GAATTAACATTCCTCTCTTCAAGAAATGCAATTAATGATGATGTTGATGATCCAGATCA 420
 Db 361 GAATTAACATTCCTCTCTTCAAGAAATGCAATTAATGATGATGTTGATGATCCAGATCA 420

QY	421	TTTGATTACAGCTCCACCAACTTACATGCTGACTATGGCTACAAAGACTGGAAACCTT	480
Dp	421	TTTATATTACAGCTCCACCAACTTACAAAGCTGACTATGGCTACAAAGACTGGAAACCTT	480
QY	481	CTCTAACCTCTCCATTTATCTAGAGCCCTTCCTCTGGCTGATGATGATTCGCCGACCTCC	540
Dp	481	CTCTAACCTCTCTCTTTTACTAGAGCCCTTCCTCTGGCTGATGATGATTCGCCGACCTCC	540
QY	541	CTTGGGTCTCAAAAGGTAAAGACAGCTTCTGATTCAAATGAGATTGGAAAAATTGCT	600
Dp	541	CTTGGGTCTCAAAAGGTAAAGACAGCTTCTGATTCAAATGAGATTGGAAAAATTGCT	600
QY	601	TCTTAAGAAGAAAGTTCAATCCCTGATATCCCAAGGCTCAAAATGATGTTTGCATTTCTTGC	660
Dp	601	TCTTAAGAAGAAAGTTCAATCCCTGATATCCCAAGGCTCAAAATGATGTTTGCATTTCTTGC	660
QY	661	CCAGACTTCACGCACACAGTTTTTTCAAACAGATCATAGAGAGGGCCAGCTTTCACCA	720
Dp	661	CCAGACTTCACGCATCAGTTTTCACAGACAGATCATAGAGAGGGCCAGCTTTCACCA	720
QY	721	CGGCTGGGCCATGGGGTGACTTAATCATATTTCACGGTAAACTCTGGCTGACACGG	780
Dp	721	CGGCTGGGCCATGGGGTGACTTAATCATATTTCACGGTAAACTCTGGCTGACACGG	780
QY	781	TAAACGGGCTTTTCAAGATGGAAAAATGAATATCAGATATATGATGATGAGAGATGTA	840
Dp	781	TAAATCGGCTTTTCAAGATGGAAAAATGAATATGATGATGATGAGAGATGTA	840
QY	841	TCCTCCACAGTCAAAAGATCTACAGGCAGAGATGATCTACCTCCTCAAGTCCCTGACCA	900
Dp	841	TCCTCCACAGTCAAAAGATCTACAGGCAGAGATGATCTACCTCCTCAAGTCCCTGACCA	900
QY	901	TCTACGTTTCTGTGGGGCAGAGGCTTTTGGTCTGGTGCCTGGTCTGATGATGATGC	960
Dp	901	TCTACGTTTCTGTGGGGCAGAGGCTTTTGGTCTGGTGCCTGGTCTGATGATGATGC	960
QY	961	CACATCTGGCTGGGGGACAAACAAGATATGATGATGCTTTAAACAGAGACATCTCGA	1020
Dp	961	CACATCTGGCTGGGGGACAAACAAGATATGATGATGCTTTAAACAGAGACATCTCGA	1020
QY	1021	ATGGGGTGATGAGCAGTGTTCACAGACAGCAGGCTAATATCTGATAGAGAGACTATTTAA	1080
Dp	1021	ATGGGGTGATGAGCAGTGTTCACAGACAGCAGGCTAATATCTGATAGAGAGACTATTTAA	1080
QY	1081	GATTGTGATTGAACATTATGTGCACAACCTTAGTGGCTATCTTCAACTGAAATTGGA	1140
Dp	1081	GATTGTGATTGAACATTATGTGCACAACCTTAGTGGCTATCTTCAACTGAAATTGGA	1140
QY	1141	CCGAGAACCTATCTTTTCAACAAACAATCCAGTACCAAAAATGATGCTGTGTAATTTAA	1200
Dp	1141	CCGAGAACCTATCTTTTCAACAAACAATCCAGTACCAAAAATGATGCTGTGTAATTTAA	1200
QY	1201	CACCCCTATCAGTCGCATCCCTCTTGCTCGACACCTTTCAAATTCAATGACCAAGAAATA	1260
Dp	1201	CACCCCTATCAGTCGCATCCCTCTTGCTCGACACCTTTCAAATTCAATGACCAAGAAATA	1260
QY	1261	CAACTATCAACAGTTTATCTACCAACACTCATATTTGTGTGAAACATGGAATTACCAGTT	1320
Dp	1261	CAACTATCAACAGTTTATCTACCAACACTCATATTTGTGTGAAACATGGAATTACCAGTT	1320
QY	1321	TGTTGAATCATTCACACAGGCAAAATTGCTGCGCAGGGTTGCTGGTGTAGAGATGTTCCACC	1380
Dp	1321	TGTTGAATCATTCACACAGGCAAAATTGCTGCGCAGGGTTGCTGGTGTAGAGATGTTCCACC	1380
QY	1381	CGCAGTACAGAAAGTATCACAGGCTTCATTTGACCACAGCAGGACAGATGAATAACAGTC	1440
Dp	1381	CGCAGTACAGAAAGTATCACAGGCTTCATTTGACCACAGCAGGACAGATGAATAACAGTC	1440
QY	1441	TTTTTAATGAGATCCGCAAAACGCTTTATGCTGTAAGCCCTTATGAAATCATTTGAGAACTTAC	1500
Dp	1441	TTTTTAATGAGATCCGCAAAACGCTTTATGCTGTAAGCCCTTATGAAATCATTTGAGAACTTAC	1500

QY	1501	AGGAGAAAAGAAATNGTCGACAGGTGGAGACACTGTATGCTGACATCCATGGCTGAG	1580
Dp	1501	AGGAGAAAAGAAATGCTGACAGGTGGAGACACTGTATGCTGACATCCATGGCTGAG	1560
QY	1561	GCTGTATCTCGCCCTTCGTGTAGAAAAGCCCTCGGCAGATGCGCATCTTGTGGTGAACCAT	1620
Dp	1561	GCTGTATCTCGCCCTTCGTGTAGAAAAGCCCTCGGCAGATGCGCATCTTGTGGTGAACCAT	1620
QY	1621	GGTGAAGTGGAGACACACTTCTCTGGAAAAGACTTATGGGTATGTTATATGTCTCC	1680
Dp	1621	GGTGAAGTGGAGACACACTTCTCTGGAAAAGACTTATGGGTATGTTATATGTCTCC	1680
QY	1681	TGCCCTACTGGAAGCGCAACACTTTGGTGGAGAAAGTGGGTTTCAAAATCAACACTGCG	1740
Dp	1681	TGCCCTACTGGAAGCGCAACACTTTGGTGGAGAAAGTGGGTTTCAAAATCAACACTGCG	1740
QY	1741	CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAAGGCGTGTCCCTTACTTCAATTCAGGT	1800
Dp	1741	CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAAGGCGTGTCCCTTACTTCAATTCAGGT	1800
QY	1801	TCCAGATCCAGAGCTCATTTAAAAACAGTCAACATCAATGCAAGTCTTCCCGCTCCGAGCT	1860
Dp	1801	TCCAGATCCAGAGCTCATTTAAAAACAGTCAACATCAATGCAAGTCTTCCCGCTCCGAGCT	1860
QY	1861	AGATGATATCAATCCCAOAGTACTATPAAAAGAAACGTCGACTGTAAGAGTCTAA	1920
Dp	1861	AGATGATATCAATCCCAOAGTACTATPAAAAGAAACGTCGACTGTAAGAGTCTAA	1920
QY	1921	TGATCATATTTATTTATTTATATGAAACAAGTGCATTTATTTATTTATTTATTTATTTT	1980
Dp	1921	TGATCATATTTATTTATTTATATGAAACAAGTGCATTTATTTATTTATTTATTTATTTT	1980
QY	1981	ATATTTAACTCCTTATGTACTTAAACATCTTCTGTAAACAGAACTCAGTACTCCTGTGCG	2040
Dp	1981	ATATTTAACTCCTTATGTACTTAAACATCTTCTGTAAACAGAACTCAGTACTCCTGTGCG	2040
QY	2041	GAGAAAGAGTCACTCTTGTGAAGACTTTATATGTCACATACTCTAAAGATTTTGTGTGCG	2100
Dp	2041	GAGAAAGAGTCACTCTTGTGAAGACTTTATATGTCACATACTCTAAAGATTTTGTGTGCG	2100
QY	2101	TGTTAACTTTGSAAAAACAGTTTAAATCTGTATTATATAACAGAGAGAAATGATTTTGA	2160
Dp	2101	TGTTAACTTTGSAAAAACAGTTTATTTCTGTTTATATAACAGAGAGAAATGATTTTGA	2160
QY	2161	CGTCTTTTACTTGAATTTCAACTTATATTTATTAAGAAGAAATGATTTGAATAC	2220
Dp	2161	CGTCTTTTACTTGAATTTCAACTTATATTTATTAAGAAGAAATGATTTGAATAC	2220
QY	2221	TTAAACACTATCACAAATGCGCAAAATGCTGAAAAGTTTATACACTGTCGATGTTCCAAAT	2280
Dp	2221	TTAAACACTATCACAAATGCGCAAAATGCTGAAAAGTTTATACACTGTCGATGTTCCAAAT	2280
QY	2281	GCATCTTCATGATGATTTGAAGATACTATGTTGAATTTTAAAGTACTTTTGGGATA	2340
Dp	2281	GCATCTTCATGATGATTTGAAGATACTATGTTGAATTTTAAAGTACTTTTGGGATA	2340
QY	2341	TTTTTCGTGATCAAAAGAAACGCGTACGTGATTTATTAAGAAATTTTAAATTTAGA	2400
Dp	2341	TTTTTCGTGATCAAAAGAAACGCGTACGTGATTTATTAAGAAATTTTAAATTTAGA	2400
QY	2401	CATTACCAAGTATTTCACTGTCTATCTTTTAAATCAGCAATGAAACAATATTTGAAATT	2460
Dp	2401	CATTACCAAGTATTTCACTGTCTATCTTTTAAATCAGCAATGAAACAATATTTGAAATT	2460
QY	2461	TCTTAATTCATAGGGTGAATCACCTGTAAAAAGCTTGTGATTTCTTAAAGTTATTTAA	2520
Dp	2461	TCTTAATTCATAGGGTGAATCACCTGTAAAAAGCTTGTGATTTCTTAAAGTTATTTAA	2520
QY	2521	CTTGTACATATTAACAAAAGAGCTGCTTGGATTTAAATCTGTAAATATGATGAAATTT	2580
Dp	2521	CTTGTACATATTAACAAAAGAGCTGCTTGGATTTAAATCTGTAAATATGATGAAATTT	2580
QY	2581	TTACTCAATTCCTGTTAAAAATTTTATTAAGTATGATGTTCTTTTACACAAAGATATA	2640

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Db      2581 TTACTCAATGCTGTGTAATAATTTTAAAGTATGTTCTTTTCCACCAAGAGTATA 2640
Qy      2641 AACCTTTTATGCTGCTGTTAAACCTCTCTTTAATCAAAATGCGCAATTTATTAAG 2700
Db      2641 AACCTTTTATGCTGCTGTTAAACCTCTCTTTAATCAAAATGCGCAATTTATTAAG 2700
Qy      2701 TGGTGGAGCCACTGCAAGTGTATCTCAAAATAAGATATCTGTTGAGATATTTCCAGAA 2760
Db      2701 TGGTGGAGCCACTGCAAGTGTATCTCAAAATAAGATATCTGTTGAGATATTTCCAGAA 2760
Qy      2761 CTGTTATATNGCTGGTAACTGTAATTAACCCCTATACCCCGCAAAAGGGTCTACCC 2820
Db      2761 CTGTTATATNGCTGGTAACTGTAATTAACCCCTATACCCCGCAAAAGGGTCTACCC 2820
Qy      2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTTATGTTCCAAATTTAGGGT 2880
Db      2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTTATGTTCCAAATTTAGGGT 2880
Qy      2881 TTAACTTTTGAAGCAACTTTTATGACCTTGTGACCTGCAAGCTGTGATCTGAGAT 2940
Db      2881 TTAACTTTTGAAGCAACTTTTATGACCTTGTGACCTGCAAGCTGTGATCTGAGAT 2940
Qy      2941 TTGCTATAGAGGTATTAAGTACCAAGCTGTGCTGATTAAGATATGTTTCTGAGAT 3000
Db      2941 TTGCTATAGAGGTATTAAGTACCAAGCTGTGCTGATTAAGATATGTTTCTGAGAT 3000
Qy      3001 TTTCCTGTTAGAGTTAATTTAGACGATCATATCATTCGCAAAAGTAGCAATGACCTC 3060
Db      3001 TTTCCTGTTAGAGTTAATTTAGACGATCATATCATTCGCAAAAGTAGCAATGACCTC 3060
Qy      3061 ATPAATATACCTCTTCAAAATGCTTAATTCATTTCAACATTAATTTATCTGAGCTTG 3120
Db      3061 ATPAATATACCTCTTCAAAATGCTTAATTCATTTCAACATTAATTTATCTGAGCTTG 3120
Qy      3121 AAGCCATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
Db      3121 AAGCCATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
Qy      3181 TTTCCTGTTAGAGTTAATTTAGACGATCATATCATTCGCAAAAGTAGCAATGACCTC 3240
Db      3181 TTTCCTGTTAGAGTTAATTTAGACGATCATATCATTCGCAAAAGTAGCAATGACCTC 3240
Qy      3241 TTTTGTGTTTACTAGTTTAAAGATCAGATTCATTTCTTGGACCTGCTGCTATATTTCT 3300
Db      3241 TTTTGTGTTTACTAGTTTAAAGATCAGATTCATTTCTTGGACCTGCTGCTATATTTCT 3300
Qy      3301 TACCTGAAGCTTTTGAAGTTTCAAGGTAAACCTCAGCTCAGAGCTGCTATTTAGCTCTC 3360
Db      3301 TACCTGAAGCTTTTGAAGTTTCAAGGTAAACCTCAGCTCAGAGCTGCTATTTAGCTCTC 3360
Qy      3361 TTAAGAGATTAATAAAAAAAAAAANG 3387
Db      3361 TTAAGAGATTAATAAAAAAAAAAANG 3387

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RESULT 4
US-08-930-589A-19

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; Sequence 19, Application US/08930589A
; Patent No. 6107087
; GENERAL INFORMATION:
; APPLICANT: MERCK FROST CANADA & CO.
; APPLICANT: O'NEILL, GARY P.
; APPLICANT: MANCINI, JOSEPH A.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; TITLE OF INVENTION: CYCLOOXYGENASE-2
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA

```

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; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,589A
; FILING DATE: 28-JUN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coppola, Joseph A
; REGISTRATION NUMBER: 38,413
; REFERENCE/DOCKET NUMBER: 19029PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-6734
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-930-589A-19

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Query Match          99.6%; Score 3374.2; DB 3; Length 3387;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3379; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy      1 GTTCAGAGAACTCTCTAGACAGCGCCCTCTTCACTCAACGCCAGACGCTCTGACAGCA 60
Db      1 GTTCAGAGAACTCTCTAGACAGCGCCCTCTTCACTCAACGCCAGACGCTCTGACAGCA 60
Qy      61 AAGCCTACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCT 120
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Db      121 GTGCGCGGCTCTGCGCGCTGAGCCATACAGCAATCTTGTCTGTCCACCAATGTCMAAA 180
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Db      181 CCGAGGTGTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
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Db      361 GAATTAACATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
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Qy      481 CTCTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
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Db      2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTTATGTTCCAAATTTAAGGT 2880
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QY      3361 TTAAGAGATTAATAAAAAAAAAAAAAAG 3387
Db      3361 TTAAGAGATTAATAAAAAAAAAAAAAAG 3387

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RESULT 5
US-09-599-781-19
: Sequence 19, Application US/09599781
: Patent No. 6362327
: GENERAL INFORMATION:
: APPLICANT: MERCK FROST CANADA & CO.
: O'NEILL, GARY P.
: MANCINI, JOSEPH A.
: TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
: CYCLOOXYGENASE-2
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESS: Merck & Co., Inc.
: STREET: P.O. Box 2000, 126 E. Lincoln Ave.
: CITY: Rahway
: STATE: NJ
: COUNTRY: USA
: ZIP: 07065-0900
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows
: SOFTWARE: PASEQU for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/599,781
: FILING DATE: 21-Jun-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/084,033

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FILING DATE: 27-Sep-1993
ATTORNEY/AGENT INFORMATION:
: NAME: Coppola, Joseph A
: REGISTRATION NUMBER: 38,413
: REFERENCE/DOCKET NUMBER: 19029PC
TELECOMMUNICATION INFORMATION:
: TELEPHONE: 732-594-6734
: TELEFAX: 732-594-4720
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3387 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-599-781-19

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Query Match      99.6% Score 3374.2; DB 4; Length 3387;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3379; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY      1 GTCCAGAACTCTCTCAGAGGCGCTCTTCAAGTCCACAGCCAGCCCTCAGACAGA 60
Db      1 GTCCAGAACTCTCTCAGAGGCGCTCTTCAAGTCCACAGCCAGCCCTCAGACAGA 60
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QY      361 GAATTAACATTCCTCTCTCTTCTGAAATGCAATTATGATGATGATGATGATGATGAT 420
Db      361 GAATTAACATTCCTCTCTCTTCTGAAATGCAATTATGATGATGATGATGATGATGAT 420
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Db 2881 TTAACCTTTTGAAGAACTTTTATGCTTGTGCACTGACAGCTGACTCAGAT 2940

QY	2941	TTTTCATAGAGTTAATGAAGTACCAAGCTGTGCTTGATTAACGATATGTTTTCTCAGAT	3000
Db	2941	TTTGCATATAGGTTATATGAAGTACCAAGCTGTGCTTGATTAACGATATGTTTTCTCAGAT	3000
QY	3001	TTTTCGTTGTACAGTTAATTATAGAGTCCATATACATTTGAAAAGTAGCAATGACCTC	3060
Db	3001	TTTTCGTTGTACAGTTAATTATAGAGTCCATATACATTTGAAAAGTAGCAATGACCTC	3060
QY	3061	ATTAATAATACCTTTCACAAATGCTTAATTCATTTTCACATTAATTTATCTCAGCTCTG	3120
Db	3061	ATTAATAATACCTTTCACAAATGCTTAATTCATTTATTCACATTTAATTTATCTCAGCTCTG	3120
QY	3121	AAGCAATTCAGTAGTGTCATTTGGAATCAAGCTGGCTAACCTGCATGCTGTCTCTTTCT	3180
Db	3121	AAGCAATTCAGTAGTGTCATTTGGAATCAAGCTGGCTAACCTGCATGCTGTCTCTTTCT	3180
QY	3181	TTTCTCTCTTTAGGCACTTTTGGTAGAGACACAGCTCTCTCAAAACACTTGTGTTCTCCTA	3240
Db	3181	TTTCTCTCTTTAGGCACTTTTGGTAGAGACACAGCTCTCTCAAAACACTTGTGTTCTCCTA	3240
QY	3241	TTTTGTTTTACTAGTTTTAAGATCAAGATTCACATTTCTTTGGAGCTGTGCTAATATTTTCT	3300
Db	3241	TTTTGTTTTACTAGTTTTAAGATCAAGATTCACATTTCTTTGGAGCTGTGCTAATATTTTCT	3300
QY	3301	TACCTGAACCTTTTGCAAGTTTTCAGGTAAACCTCAGCTCAGAGACTGCTAATTTAGCTCTC	3360
Db	3301	TACCTGAACCTTTTGCAAGTTTTCAGGTAAACCTCAGCTCAGAGACTGCTAATTTAGCTCTC	3360
QY	3361	TTAAGAGATTTAAAAAAG 3387	
Db	3361	TTAAGAGATTTAAAAAAG 3387	

RESULT 6

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US-08-487-753-3
: Sequence 3, Application US/08487753
: Patent No. 5807733
: GENERAL INFORMATION:
: APPLICANT: Young, Donald A.
: APPLICANT: O'Banion, Michael K.
: APPLICANT: Winn, Virginia D.
: TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
: NUMBER OF INVENTION: FUSION PROTEINS
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,753
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 3996-011
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1834 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single

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;      TOPOLOGY: unknown
;      MOLECULE TYPE: DNA (genomic)
US-08-487-753-3

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Query Match	53.2%	Score 1803.2;	DB 1;	Length 1834;
Best Local Similarity	99.0%;	Pred. No. 0;		
Matches 1814; Conservative	0;	Mismatches 18;	Indels 0;	Gaps 0;

QY	90	CCGCTGCGATGCTGCCGCCGCCCGCCCTGCTGTCGCGCGGCTCGGCGCTCAGCCATACAG	149
Db	1	CCGCTGGAGATGCTGCCGCCGCCCGCCCTGCTGTCGCGCGGCTCGGCGCTCAGCCATACAG	60
QY	150	CAAAATCCTTGCTGTTCACCACTGTCAAAACCGAGGTGTATGTAGTGTGGATTGG	209
Db	61	CAAAATCCTTGCTGTTCACCACTGTCAAAACCGAGGTGTATGTAGTGTGGATTGG	120
QY	210	ACGAGATATAGTGCAGATGTGATCCCGGACAGAGATCTATGTAGAAAACTCTCAACCGG	269
Db	121	ACGAGATATAGTGCAGATGTGATCCCGGACAGAGATCTATGTAGAAAACTCTCAACCGG	180
QY	270	AATTTTGAACAAGATTAATAATTTCTGAAAACCACTCCAAACACAGTGCATACATAC	329
Db	181	AATTTTGAACAAGATTAATAATTTCTGAAAACCACTCCAAACACAGTGCATACATAC	240
QY	330	TTAACCACTTCAAGGGAATTTTGAAAGCTTGTGAATTAACATTCCTTCTTGAAATGCA	389
Db	241	TTAACCACTTCAAGGGAATTTTGAAAGCTTGTGAATTAACATTCCTTCTTGAAATGCA	300
QY	390	TTATGAGTATGTGTGATGCATGCATGCATCACTTGTGTTACAGTGCACCACTTACATG	449
Db	301	TTATGAGTATGTGTGATGCATGCATGCATCACTTGTGTTACAGTGCACCACTTACATG	360
QY	450	CTGACTATGTGCTACAAAAGCTGGGAAGCCTTCTTAACCTCTCTATTATATCTAGAGCC	509
Db	361	CTGACTATGTGCTACAAAAGCTGGGAAGCCTTCTTAACCTCTCTATTATATCTAGAGCC	420
QY	510	TTCTCTCGTGCCTGATGATTTGCGCGACCTCCCTTGGGTGTCAAAGTAAAAAGCATTC	569
Db	421	TTCTCTCGTGCCTGATGATTTGCGCGACCTCCCTTGGGTGTCAAAGTAAAAAGCATTC	480
QY	570	CTGATTTCAAAATGAGATTTGTGAAAAATTTGCTTTTAAAGAAAGATCAATCCCTGATCCC	629
Db	481	CTGATTTCAAAATGAGATTTGTGAAAAATTTGCTTTTAAAGAAAGATCAATCCCTGATCCC	540
QY	630	AGGCGTCAAACTATGATGTTTGGATTCTTTGCCAGCACTTCAACGACCAAGTTTTCAGA	689
Db	541	AGGCGTCAAACTATGATGTTTGGATTCTTTGCCAGCACTTCAACGATCAGTTTTCAGA	600
QY	690	CAGATCATACAGAGGCGCAGCTTCAACCAAGGCGTGGGCAATGGGTTGACTTAATC	749
Db	601	CAGATCATACAGAGGCGCAGCTTCAACCAAGGCGTGGGCAATGGGTTGACTTAATC	660
QY	750	ATAATTACGCTGAAACTCTGCTAGACAGCGTAAATCTGCGCTTTTCAAGATGAAAAA	809
Db	661	ATAATTACGCTGAAACTCTGCTAGACAGCGTAAATCTGCGCTTTTCAAGATGAAAAA	720
QY	810	TGAATATACATATTAATGATGAGAAAGATGATCTCTCCCAACAGTCAAAAGATCTACAGCAG	869
Db	721	TGAATATACATATTAATGATGAGAAAGATGATCTCTCCCAACAGTCAAAAGATCTACAGCAG	780
QY	870	AGATGATCTACCTCTCTCAAGTCCCTAGACATCTACGATCTCTGCTGTGGGCGAGAGGCT	929
Db	781	AGATGATCTACCTCTCTCAAGTCCCTAGACATCTACGATCTCTGCTGTGGGCGAGAGGCT	840
QY	930	TTGGTCTGTGCTCTGTGCTGTGATGATGATGACACATCTGCTGCGGAAACACAACAGAG	989
Db	841	TTGGTCTGTGCTCTGTGCTGTGATGATGATGACACATCTGCTGCGGAAACACAACAGAG	900
QY	990	TATGTGATGTGCTTAAACAGAGAGATCTTAATGGGGTGTATGAGCAATTTTCCAGACAA	1049
Db	901	TATGTGATGTGCTTAAACAGAGAGATCTTAATGGGGTGTATGAGCAATTTTCCAGACAA	960
QY	1050	GCAGGCTTAATCTGATGTGAGAGACTAATTAAAGTTGTGATTTAGAAATTAATGTCAACACT	1109


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Db      961  GCAGGCTAAATACGATAGAGAGACTATTGAATTGATTGAAGATTGATGCAACT 1020
QY      1110  TGAATGCTCTGCTCACTTCAAACTGAAATTTGACCAGAACTACTTTCAACAACTTCC 1169
Db      1021  TGAATGCTCTGCTCACTTCAAACTGAAATTTGACCAGAACTACTTTCAACAACTTCC 1080
QY      1170  AGTACCAAAATCGTATTGCTGCTGAATTTAACACCTCTATCTACTGGCACTCCCTTGC 1229
Db      1081  AGTACCAAAATCGTATTGCTGCTGAATTTAACACCTCTATCTACTGGCACTCCCTTGC 1140
QY      1230  CTGACACTTTCGAATTCATGACACGAAATGAACTATCAAGCTTATATGACAACT 1289
Db      1141  CTGACACTTTCGAATTCATGACACGAAATGAACTATCAAGCTTATATGACAACT 1200
QY      1290  CTATATGCTGGAACATGAAATTTACCAAGTTTGTGAATCTTACCAAGCAATTCCTG 1349
Db      1201  CTATATGCTGGAACATGAAATTTACCAAGTTTGTGAATCTTACCAAGCAATTCCTG 1260
QY      1350  GCAGGCTTGTCTGTGTGAGAAATTTCCACCCGAGTACAGAAATGATCAGAGCTTCCA 1409
Db      1261  GCAGGCTTGTCTGTGTGAGAAATTTCCACCCGAGTACAGAAATGATCAGAGCTTCCA 1320
QY      1410  TTGACCAAGAGGAGGAGTGAATATCCAGTCTTTTATGAGTACCGAAAGCTTTATGC 1469
Db      1321  TTGACCAAGAGGAGGAGTGAATATCCAGTCTTTTATGAGTACCGAAAGCTTTATGC 1380
QY      1470  TGAAGCCCTTATGAAATCTTTGAGAACTTACAGAGAAAGAAATGTCTGCAAGTTGG 1529
Db      1381  TGAAGCCCTTATGAAATCTTTGAGAACTTACAGAGAAAGAAATGTCTGCAAGTTGG 1440
QY      1530  AAGCACTCTATGATGATCATGCTGTGTGAGCTGTATCTCCCTTCTGTTAGAAAGC 1589
Db      1441  AAGCACTCTATGATGATCATGCTGTGTGAGCTGTATCTCCCTTCTGTTAGAAAGC 1500
QY      1590  CTGGGCGAGATGCACTCTTGTGTAACAGTGAAGTTGAGAACCACTTCTCTTGA 1649
Db      1501  CTGGGCGAGATGCACTCTTGTGTAACAGTGAAGTTGAGAACCACTTCTCTTGA 1560
QY      1650  AAGCACTTATGAGTATATCTTATATCTTCTCTGCTACTGGAAGCAAGCACTTTGCTG 1709
Db      1561  AAGCACTTATGAGTATATCTTATATCTTCTCTGCTACTGGAAGCAAGCACTTTGCTG 1620
QY      1710  GAGAAATGAGTTTAAATCATCAACATGCTCTCAATTCAGTCTCTGATCTGCAATAG 1769
Db      1621  GAGAAATGAGTTTAAATCATCAACATGCTCTCAATTCAGTCTCTGATCTGCAATAG 1680
QY      1770  TGAAGGCGTGTCCCTTCACTTCACTGAGTCTCCAGATCCAGAGCTCATTAACAGTCA 1829
Db      1681  TGAAGGCGTGTCCCTTCACTTCACTGAGTCTCCAGATCCAGAGCTCATTAACAGTCA 1740
QY      1830  CCATCAATGCAAGTCTTCCGCGCTCCGCACTAGATGATATCAATCCACAGTACTTAA 1889
Db      1741  CCATCAATGCAAGTCTTCCGCGCTCCGCACTAGATGATATCAATCCACAGTACTTAA 1800
QY      1890  AAGAACGCTGCACTGATCTGTGAAGTCTAAT 1921
Db      1801  AAGAACGCTGCACTGATCTGTGAAGTCTAAT 1832

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RESULT 7

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US-08-487-753-14
; Sequence 14, Application US/08487753
; Patent No. 5807733
; GENERAL INFORMATION:
; APPLICANT: Young, Donald A.
; APPLICANT: O'Banion, Michael K.
; APPLICANT: Winn, Virginia D.
; TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds

```

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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,753
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3996-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1834 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-487-753-14

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Query Match          53.2%; Score 1803.2; DB 1; Length 1834;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1814; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY      90  CCAGTGGAGTCTGCGCCGCGCTGCTGCTGTGCGGCTCTGCGCTGAGCCATACAG 149
Db      1  CCGCTGGAGTCTGCGCCGCGCTGCTGCTGTGCGGCTCTGCGCTGAGCCATACAG 60
QY      150  CAATTCCTGTGTCTCCACCCATGTCAAAACGAGGATGATATGATAGTGGGATTTG 209
Db      61  CAATTCCTGTGTCTCCACCCATGTCAAAACGAGGATGATATGATAGTGGGATTTG 120
QY      210  ACCAGTATAGTGGATGTGACCCGAGAGATTTATGAGAAATGCTCAACACCGG 269
Db      121  ACCAGTATAGTGGATGTGACCCGAGAGATTTATGAGAAATGCTCAACACCGG 180
QY      270  AATTTTGAACAAGATTAATTTTCTGAAACCCAGCTCCAAACAGAGTGAATACATC 329
Db      181  AATTTTGAACAAGATTAATTTTCTGAAACCCAGCTCCAAACAGAGTGAATACATC 240
QY      330  TTACCACTTCAAGGATTTTGAACGTTGGAATTAATTCCTTCTGAAATGCA 389
Db      241  TTACCACTTCAAGGATTTTGAACGTTGGAATTAATTCCTTCTGAAATGCA 300
QY      390  TTATGATGATGTGTGAATCATGACATGATCAATTTGATGACAGTCCACCACTTCAATG 449
Db      301  TTATGATGATGTGTGAATCATGACATGATCAATTTGATGACAGTCCACCACTTCAATG 360
QY      450  CTGACTATGCTACAAAGAGTGGGAAAGCTTCTCTTAACTCTCTTATATATCTAGAGCC 509
Db      361  CTGACTATGCTACAAAGAGTGGGAAAGCTTCTCTTAACTCTCTTATATATCTAGAGCC 420
QY      510  TTCCCTCTGCTGCTATGATGCTCCGCACTCCCTGGGAGTCAAGAGTAAAGAGCTTC 569
Db      421  TTCCCTCTGCTGCTATGATGCTCCGCACTCCCTGGGAGTCAAGAGTAAAGAGCTTC 480
QY      570  CTGATTCAAATGAGATTTGGAAGAAATGCTTTTGAAGAAAGATTCATCCTGATCCCC 629
Db      481  CTGATTCAAATGAGATTTGGAAGAAATGCTTTTGAAGAAAGATTCATCCTGATCCCC 540
QY      630  AGGAGTCAAAATGATGTTGATTTGCTTTGCGCAGACTTTCAGACAGTCTTTTCAAGA 689

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QY 270 AATTTTGAAGATTAATTTATTTCTGAACCCACTTCCAAACACAGTGCATCTATAC 323
 Db 181 AATTTTGAAGATTAATTTATTTCTGAACCCACTTCCAAACACAGTGCATCTATAC 240
 QY 330 TTACCACTTCAAGGATTTTGAAGCTTGTGAATATACATTCCTCTCCATGCAATGCA 389
 Db 241 TTACCACTTCAAGGATTTTGAAGCTTGTGAATATACATTCCTCTCCATGCAATGCA 300
 QY 390 TTATAGTTATGTGTGAATCAGATCAATTTGATGACAGTCCACCACTTATCAATG 449
 Db 301 TTATAGTTATGTGTGAATCAGATCAATTTGATGACAGTCCACCACTTATCAATG 360
 QY 450 CTGATATAGCTGACAAAGCTGGGAAGCTTCTAACCTCTCCATTAATATAGAGCC 509
 Db 361 CTGATATAGCTGACAAAGCTGGGAAGCTTCTAACCTCTCCATTAATATAGAGCC 420
 QY 510 TTCCCTCGTGCCTGATGATGCGGACTCCCTTGGGATGTCAAAGATTAAGAGCTTC 569
 Db 421 TTCCCTCGTGCCTGATGATGCGGACTCCCTTGGGATGTCAAAGATTAAGAGCTTC 480
 QY 570 CTGATTTCAATGAGATTTGTGAAAAATGCTTCTAAGAAAGATTCATCCCTGATCCC 629
 Db 481 CTGATTTCAATGAGATTTGTGAAAAATGCTTCTAAGAAAGATTCATCCCTGATCCC 540
 QY 630 AGGCTCAAAACATGATGTTGATCTTGGCCAGACCTTCACGACAGCACTTTTCAAGA 689
 Db 541 AGGCTCAAAACATGATGTTGATCTTGGCCAGACCTTCACGACAGCACTTTTCAAGA 600
 QY 690 CAGATCATAGCGAGGCGAGCTTTCACCAACGAGCTGGGCTGAGGATGGAATTAAATC 749
 Db 601 CAGATCATAGCGAGGCGAGCTTTCACCAACGAGCTGGGCTGAGGATGGAATTAAATC 660
 QY 750 ATATTGAGGTGAATCTGCTGCTAAGACGCTAAATCTGCGCTTTTCAAGATGGAATAA 809
 Db 661 ATATTGAGGTGAATCTGCTGCTAAGACGCTAAATCTGCGCTTTTCAAGATGGAATAA 720
 QY 810 TGAATATCAGATTAATGATGAGAGATGATCTCCCAACAGTCAAGATCTCAGGACG 869
 Db 721 TGAATATCAGATTAATGATGAGAGATGATCTCCCAACAGTCAAGATCTCAGGACG 780
 QY 870 AGATGATCTACCTCTCTCAAGTCCCTGAGCATCTACGTTTCTGCTGAGGACAGAGTCT 929
 Db 781 AGATGATCTACCTCTCTCAAGTCCCTGAGCATCTACGTTTCTGCTGAGGACAGAGTCT 840
 QY 930 TTGCTGCTGCTGCTGCTGATGATGATGCAATCTGCTGCGGGAACACAAACAGAG 989
 Db 841 TTGCTGCTGCTGCTGCTGATGATGATGCAATCTGCTGCGGGAACACAAACAGAG 900
 QY 990 TATGATGATGCTGTTAAACAGAGCATCCGATGAGGAGTGAAGAGATGTTCCAGACA 1049
 Db 901 TATGATGATGCTGTTAAACAGAGCATCCGATGAGGAGTGAAGAGATGTTCCAGACA 960
 QY 1050 GCAGGCTAATATCTGATAGAGAGACATTAATGATGATGATGATGATGATGATGAT 1109
 Db 961 GCAGGCTAATATCTGATAGAGAGACATTAATGATGATGATGATGATGATGATGAT 1020
 QY 1110 TGAAGTGGCTATCACTTCAAACTGAAATTTGACCCAGAACTACTTTTCAACAACTTC 1169
 Db 1021 TGAAGTGGCTATCACTTCAAACTGAAATTTGACCCAGAACTACTTTTCAACAACTTC 1080
 QY 1170 AGTACCAAAATGATGATGCTGCTGATTAACACCTCTATACAGGAGCTATCCCTTCTGC 1229
 Db 1081 AGTACCAAAATGATGATGCTGCTGATTAACACCTCTATACAGGAGCTATCCCTTCTGC 1140
 QY 1230 CTGACACCTTCAAAATCTGACAGAAATATACAACTATCAAGATTTATCTCAACAACT 1289
 Db 1141 CTGACACCTTCAAAATCTGACAGAAATATACAACTATCAAGATTTATCTCAACAACT 1200
 QY 1290 CTATATGCTGGAACATGGAATTTACCAAGTGTGTAATCATTTACACAGGCAATTTGCTG 1349
 Db 1201 CTATATGCTGGAACATGGAATTTACCAAGTGTGTAATCATTTACACAGGCAATTTGCTG 1260

QY 1350 GCAGGCTTGTGATGAGAAATGTTCCACCCGAGTACAGAAAGTATCACAGGCTTCCA 1409
 Db 1261 GCAGGCTTGTGATGAGAAATGTTCCACCCGAGTACAGAAAGTATCACAGGCTTCCA 1320
 QY 1410 TTGACACAGAGCAGAGTGAATTAACAGTCTTTTAATGATGATGATGATGATGATGAT 1469
 Db 1321 TTGACACAGAGCAGAGTGAATTAACAGTCTTTTAATGATGATGATGATGATGATGAT 1380
 QY 1470 TGAAGCTTATGATCACTTTGAAGACTTACAGAGAAAGAAATGTTCTGAGATG 1529
 Db 1381 TGAAGCTTATGATCACTTTGAAGACTTACAGAGAAAGAAATGTTCTGAGATG 1440
 QY 1530 AAGCACTATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1589
 Db 1441 AAGCACTATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 QY 1590 CTGGCCAGATGCCATCTTTGATGAAACATGATGATGATGATGATGATGATGATGATGAT 1649
 Db 1501 CTGGCCAGATGCCATCTTTGATGAAACATGATGATGATGATGATGATGATGATGATGAT 1560
 QY 1650 AAGCACTATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1709
 Db 1561 AAGCACTATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 QY 1710 GAGAAGTGGTTTTCAATCAATCAACACTGCTCAATCAATCAATCAATCAATCAATCAAT 1769
 Db 1621 GAGAAGTGGTTTTCAATCAATCAACACTGCTCAATCAATCAATCAATCAATCAATCAAT 1680
 QY 1770 TGAAGGCTGCTGCTTCACTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1829
 Db 1681 TGAAGGCTGCTGCTTCACTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1740
 QY 1830 CCATCAATGCAAGTCTTCCGCTCCGAGCTAGATGATGATGATGATGATGATGATGATGAT 1889
 Db 1741 CCATCAATGCAAGTCTTCCGCTCCGAGCTAGATGATGATGATGATGATGATGATGATGAT 1800
 QY 1890 AAGAACGCTGCACTGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1921
 Db 1801 AAGAACGCTGCACTGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1832

RESULT 9
 US-08-480-065-14
 ; Sequence 14, Application US/08480065
 ; Patent No. 5837479
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Donald A.
 ; APPLICANT: O'Banion, Michael K.
 ; APPLICANT: Winn, Virginia D.
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR INHIBITORS OF
 ; MAMMALIAN PROTAGLANDIN H SYNTHASE-2
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,065
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cornuzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 3996-012
 ; TELECOMMUNICATION INFORMATION:

QY	1230	TGACACGCTTTGCAATTCAGACACGAAATACACTATCAAGCTTTATCTACAACACT	1289
Db	1141	CTGACACGCTTTGCAATTCAGACACGAAATACACTATCAAGCTTTATCTACAACACT	1200
QY	1290	CTATATTTGCTGGAACATGGAATTAACCCAGTTTGTGTAATCATTCACGAGCAATTTCTG	1349
Db	1201	CTATATTTGCTGGAACATGGAATTAACCCAGTTTGTGTAATCATTCACGAGCAATTTCTG	1260
QY	1350	GCAGGGTTTGCTGTGTGTAGAAATGTTCCACCCGAGTACAGAAATGTATCAAGGCTTCCA	1409
Db	1261	GCAGGGTTTGCTGTGTGTAGAAATGTTCCACCCGAGTACAGAAATGTATCAAGGCTTCCA	1320
QY	1410	TTGACCCAGACGAGCGAGATGAAATACCAAGTCTTTTAATGAGTACCGCAAAACGCTTTATGC	1469
Db	1321	TTGACCCAGACGAGCGAGATGAAATACCAAGTCTTTTAATGAGTACCGCAAAACGCTTTATGC	1380
QY	1470	TGAAAGCCCTATGATTCATTTTGAAACACTTCACAGAGAAAGAAATGTCTGCAAGTTGG	1529
Db	1381	TGAAAGCCCTATGATTCATTTTGAAACACTTCACAGAGAAAGAAATGTCTGCAAGTTGG	1440
QY	1530	AAGCACTCTATGTGTGACATCGATGCTGTGAGCTGTATCTGCCCTTCTGGTAGAAAAAC	1589
Db	1441	AAGCACTCTATGTGTGACATCGATGCTGTGAGCTGTATCTGCCCTTCTGGTAGAAAAAC	1500
QY	1590	CTGGGCCAGATGCCATCTTTTGTGTAAACCATGTGTAGAAAGTTGGAGACACTTCCTCTGA	1649
Db	1501	CTGGGCCAGATGCCATCTTTTGTGTAAACCATGTGTAGAAAGTTGGAGACACTTCCTCTGA	1560
QY	1650	AAGCACTTATGGGTAAATGTTATATGTTCTCTGCTACTGTGAAGCCAAAGCACTTTTGGTG	1709
Db	1561	AACCACTTATGGGTAAATGTTATATGTTCTCTGCTACTGTGAAGCCAAAGCACTTTTGGTG	1620
QY	1710	GAGAAAGTGGGTTTTCAAAATCATCAACACTGCTCAATTCAGTCTCTCATCTGCAATTAAC	1769
Db	1621	GAGAAAGTGGGTTTTCAAAATCATCAACACTGCTCAATTCAGTCTCTCATCTGCAATTAAC	1680
QY	1770	TGAAAGGGGTGTCCTTTACTTCATTCAGGTCCAGATCCAGATCCAGAGCTCATTTAAACAGTCA	1829
Db	1681	TGAAAGGGGTGTCCTTTACTTCATTCAGGTCCAGATCCAGATCCAGAGCTCATTTAAACAGTCA	1740
QY	1830	CCATCAATGCAAGTTCTTCCCGCTCCGACGTAGATGATATCAATCCACAGTATCTATCTTA	1889
Db	1741	CCATCAATGCAAGTTCTTCCCGCTCCGACGTAGATGATATCAATCCACAGTATCTATCTTA	1800
QY	1890	AAGAAAGCTGCAGCTGACCTGTAGAAAGTCTAAT	1921
Db	1801	AAGAAAGCTGCAGCTGACCTGTAGAAAGTCTAAT	1832

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1      RESULT 12
2      PCT-US93-09167-3
3      Sequence 3, Application PC/TUS9309167
4      GENERAL INFORMATION:
5      APPLICANT: Young, Donald A.
6      APPLICANT: O'Banion, M. Kerry
7      APPLICANT: Winn, Virginia D.
8      TITLE OF INVENTION: Steadily-Transformed Mammalian Cells
9      TITLE OF INVENTION: Expressing a Regulated, Inflammatory Cyclooxygenase
10     NUMBER OF SEQUENCES: 13
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Merchant & Gould
13     STREET: 3100 Norwest Center
14     CITY: Minneapolis
15     STATE: MN
16     COUNTRY: USA
17     ZIP: 55402
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: PatentIn Release #1.0, Version #1.25
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: PCT/US93/09167

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FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Moessner, Warren D.
 REGISTRATION NUMBER: 30,440
 REFERENCE/DOCKET NUMBER: 6840-20-US-01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-332-5300
 TELEFAX: 612-332-9081
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1834 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Human PCHS-2

Query Match	53.2%	Score 1003.2	DB 5	Length 1834
Best Local Similarity	99.0%	Pred. No. 0		
Matches 1814; Conservative	0	Mismatches 18	Indels 0	Gaps 0

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Qy	150	CAATTCCTGCTGTTCCACCCCATGTCAAAACGAGGTGTATGTATGTAGTGTGGATTTTG	209
Db	61	CAATTCCTGCTGTTCCACCCCATGTCAAAACGAGGTGTATGTATGTAGTGTGGATTTTG	120
Qy	210	ACGAGTATTAAGTGGATTTGTACCCGGACAGGATTCATATGAGGAAAACTGTCTCAACCGG	269
Db	121	ACGAGTATTAAGTGGATTTGTACCCGGACAGGATTCATATGAGGAAAACTGTCTCAACCGG	180
Qy	270	AATTTTGAACAAGAAATAAATTTATTTCTGAAGAACCACTCCAAACACAGTGCATCAATAC	329
Db	181	AATTTTGAACAAGANTAAATATTTATTTCTGAAGAACCACTCCAAACACAGTGCATCAATAC	240
Qy	330	TTACCCACTTCAAGGGATTTTGGACGTTGTGATATACATTCCTCTTGCAATGCAAC	389
Db	241	TTACCCACTTCAAGGGATTTTGGACGTTGTGATATACATTCCTCTTGCAATATGCAAC	300
Qy	390	TTATGAGTTATGTGTGTGACATCCAGATCAACTGATTTGACAGAGTCCACCACTTCAATG	449
Db	301	TTATGAGTTATGTGTGTGACATCCAGATCAACTGATTTGACAGAGTCCACCACTTCAATG	360
Qy	450	CTGACTATGGCTACAAAGCTGGGAAGCTTCTCAACCTCTCATTTATATACATGAGCCC	509
Db	361	CTGACTATGGCTACAAAGCTGGGAAGCTTCTCAACCTCTCATTTATATACATGAGCCC	420
Qy	510	TTCTCTCTGTGCTGATGATTTGCCGCACTCCCTTG3GTGTCAAAAGTAAAAAGCAGCTTC	569
Db	421	TTCTCTCTGTGCTGATGATTTGCCGCACTCCCTTG3GTGTCAAAAGTAAAAAGCAGCTTC	480
Qy	570	CTGATTTCAATTAAGATTTGTGAAAAAATTCCTCTTAAGAAAGAAAGTCAATCCCGATCCCC	629
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Qy	630	AGGGCTCAAAACATGATGTTGTGATCTTTTGCCAGCACTTCACGCAACAGTTTTTCAAG	689
Db	541	AGGGCTCAAAACATGATGTTGTGATCTTTTGCCAGCACTTCACGCAACAGTTTTTCAAG	600
Qy	690	CAGATCATTAAGCAGAGGCGCAGCTTTCACCAACGAGCTGGGCCATATGGGGTGTGACTTAATTC	749
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Qy	750	AATATTTAGCGTGAATCTTGGCTGACACAGCTTAACTGGCGCTTTTCAAGGATGAGAAAA	809
Db	661	AATATTTAGCGTGAATCTTGGCTGACACAGCTTAACTGGCGCTTTTCAAGGATGAGAAAA	720
Qy	810	TGAAATATGAGTAATTTGATGGAAGATGTATCTCCACACATCAAGATACTACAGCAG	865

Db 721 TGAATATCAGATTAATTGAGAGATGATCTTCCACAGTCAAAAGTACTCAGGCGAG 780
 Qy 870 AGATGATCTAACCTCTCAAGTCCCTGAGCATCTACGTTTGTGCGGAGAGAGTCT 929
 Db 781 AGATGATCTAACCTCTCAAGTCCCTGAGCATCTACGTTTGTGCGGAGAGAGTCT 840
 Qy 930 TTGGTGTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 989
 Db 841 TTGGTGTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Qy 990 TATGATGATGCTTAAACAGAGACATCCGAAATGGGGGTATGAGAGTGTTCAGACAA 1049
 Db 901 TATGATGATGCTTAAACAGAGACATCCGAAATGGGGGTATGAGAGTGTTCAGACAA 960
 Qy 1050 GAGGCTTAATCTGATAGAGAGACTATTAGATTGTGATGATGATGATGATGATGAT 1109
 Db 961 GAGGCTTAATCTGATAGAGAGACTATTAGATTGTGATGATGATGATGATGATGAT 1020
 Qy 1110 TGAGTGGCTATCTCACTTCAAACTGAAATTTGACCCGAACTACTTTTCAACAAAGATCC 1169
 Db 1021 TGAGTGGCTATCTCACTTCAAACTGAAATTTGACCCGAACTACTTTTCAACAAAGATCC 1080
 Qy 1170 AGTACCAAAATCGTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1229
 Db 1081 AGTACCAAAATCGTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1140
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 Db 1621 GAGAAGTGGTGTTCATCAATCAACATGCTCAATCAATCAATCAATCAATCAATCAAT 1680
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 Qy 1890 AAGAACGCTGACTGAACTGTAAGTCTTAAT 1921

Db 1801 AAGAACGCTGCACTGTAAGTCTTAAT 1832
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 US-09-919-060-4
 ; Sequence 4, Application US/09919060
 ; Patent No. 6638744
 ; GENERAL INFORMATION:
 ; APPLICANT: Wisniewski, Nancy
 ; APPLICANT: Brandt, Kevin S.
 ; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
 ; FILE REFERENCE: AD-1
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: 60/224,486
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 3509
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (53)..(1864)
 ; OTHER INFORMATION:
 US-09-919-060-4

Query Match 47.9%; Score 1621.6; DB 4; Length 3509;
 Best Local Similarity 84.0%; Pred. No. 0;
 Matches 1935; Conservative 0; Mismatches 314; Indels 55; Gaps 7;

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 Db 14 CACG 73
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 Qy 179 AACCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 238
 Db 134 AACCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 193
 Qy 239 GGAATCTATGAGAGAAATCTGCTCAACACCGGAATTTTGGACAAATTAATTTCTG 298
 Db 194 GGAATCTATGAGAGAAATCTGCTCAACACCGGAATTTTGGACAAATTAATTTCTG 253
 Qy 299 AAACCACTCCAAACACAGTGCATGATGATGATGATGATGATGATGATGATGATGAT 358
 Db 254 AAACCACTCCAAACACAGTGCATGATGATGATGATGATGATGATGATGATGATGAT 313
 Qy 359 GTGAATTAATTCCTCTCTTGGAAATGCAATTAATGATGATGATGATGATGATGATGAT 418
 Db 314 GTGAATTAATTCCTCTCTTGGAAATGCAATTAATGATGATGATGATGATGATGATGAT 373
 Qy 419 CATTTATGAGAGGTCACCAATTAATGATGATGATGATGATGATGATGATGATGATGAT 478
 Db 374 CATTTATGAGAGGTCACCAATTAATGATGATGATGATGATGATGATGATGATGATGAT 433
 Qy 479 TTCTTAACCTCTCTATTAATTAAGAGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCT 538
 Db 434 TTCTTAACCTCTCTATTAATTAAGAGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCT 493
 Qy 539 CCCTTGGGCTCAAGGTTAAAGAGAGCTTCTGATTAATGATGATGATGATGATGATGAT 598
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 Qy 599 CTCTTAAGAGAAAGTTCAATCCCTGATCCCGAGGCTCAACATGATGATGATGATGAT 658
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Db      794  TATCTCTCAACCGTCAAGATTAATCAAGCAGAGATGATCTACCTCAAGTCTCTGAG 853
QY      899  CATCTACGGTTTGTGTGGGGCAGAGAGTCTTGGTCTGTGGTCTGTGATGATGAT 958
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QY      959  GCCCAATCTGGCTGGGGGAAACAACAGATATGTATGTGCTTAAACAGAGCATCT 1018
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QY      1019  GAATGGGGTATGAGCAGATGTTGTTCAAGACAGAGCTAATATGATAGAGAGATAT 1078
Db      974  GAATGGGATGATGAGCGGTTATTCAGACAGAGCTTAATCTTATGAGAAACAT 1033
QY      1079  AAGATTTGATGAGATTAATGATGACACATTTAGTGGCTATCACTTCAAACTGAAT 1138
Db      1034  AAGATTTGATGAGATTAATGATGACACATTTAGTGGCTATCACTTCAAACTGAAT 1093
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QY      1199  AACACCTCTATCACTGGGATCCCTTGTGCTGACACCTTTCAAATTCATGACCA 1258
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QY      1259  TACAACTATCAACAGTTTATCTACAACTCTATATGCTGGAACATGAAATTCAG 1318
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QY      1859  CTAGATATATCAATCCCAAGTACTACTTAAAGAAAGCGTGAAGTGAAGTGAAGTCT 1918
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QY      1919  AATGATCAATTTATTTATTTATATGAACCATGCTATTTATTTATTTATTTATTTAT 1978
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QY      1979  TTATATTAATCTCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2038
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QY      2039  CGGAGAAAGAGTCAATCTGTGGAAGCTTTATGTCATCTACTTAAAGATTTGCTGT 2098
Db      1967  AGGAGAAAGAGGTCATCTGTGGAAGCTTTATGTCATCTACTTAAAGATTTGCTGT 2021
QY      2099  GCTGTAAAGTTTGAAGAAAGCTTTTATTTGCTTTTATTTAAACAGAGAGAAATGAT 2158
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QY      2159  GAGCTCTTTTACTTGATTTCACTTATTTATTTATTTATTTATTTATTTATTTATTT 2215
Db      2066  GACATCTTTTACTTGATTTCACTTATTTATTTATTTATTTATTTATTTATTTATTT 2125
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Db      2186  ATTTCTATGATCTTCCCTGCTGATTAAGAGAACTACCTGCAACCTTCTTTCTTC 2245
QY      2332  TTTGGGATTTTCTGTCAATCA 2355
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RESULT 14
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; Sequence 6, Application US/09919060
; Patent No. 6638744
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
; FILE REFERENCE: AD-1
; CURRENT APPLICATION NUMBER: US/09/919, 060
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/224,486
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 6
; LENGTH: 3509
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-919-060-6

Query Match      47.9%; Score 1621.6; DB 4; Length 3509;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 1935; Conservative 0; Mismatches 314; Indels 55; Gaps 7;

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Db      3496  CACCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 3437
QY      119  CTGTGGCGGCTCTGCGCTGACCATTAAGCAATCTTGTCTTCCACCATGTCAT 178

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 11:20:32 ; Search time 1301 Seconds

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Title: US-08-064-271-11

Perfect score: 3387
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Scoring table:

IDENTITY NUC
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Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications NA:*

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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3379	99.8	3387	16	US-10-191-997-87 Sequence 87, Appl
2	3374.2	99.6	3387	15	US-10-027-961A-19 Sequence 19, Appl
3	3216.6	95.0	4465	10	US-09-953-067A-2 Sequence 2, Appl
4	3216.6	95.0	4465	13	US-10-211-462-132 Sequence 132, Appl
5	3216.6	95.0	4465	13	US-10-170-385-238 Sequence 238, Appl
6	3216.6	95.0	4465	15	US-10-021-660-442 Sequence 42, Appl
7	3216.6	95.0	4465	16	US-10-295-027-31 Sequence 31, Appl
8	3216.6	95.0	4465	16	US-10-373-801-11 Sequence 11, Appl
9	3215	94.9	4496	14	US-10-044-090-478 Sequence 478, Appl
10	3215	94.9	4496	14	US-10-071-766-46 Sequence 46, Appl
11	3215	94.9	4750	15	US-10-247-671-126 Sequence 126, Appl
12	2513.4	74.2	2563	14	US-10-044-090-477 Sequence 477, Appl
13	1727	51.0	9453	9	US-09-954-456-324 Sequence 25, Appl
14	1717.4	50.7	11064	10	US-09-949-293-25 Sequence 25, Appl

15	1621.6	47.9	3509	9	US-09-919-060-4	Sequence 4, Appl
16	1621.6	47.9	3509	9	US-09-919-060-6	Sequence 6, Appl
17	1525.8	45.0	3986	10	US-09-953-067A-6	Sequence 7, Appl
18	1476.6	43.6	1812	9	US-09-919-060-7	Sequence 8, Appl
19	1476.6	43.6	1812	9	US-09-919-060-8	Sequence 103, Appl
20	1431.8	42.3	4404	16	US-10-191-803-103	Sequence 13, Appl
21	727.6	21.5	1807	13	US-10-382-248-5	Sequence 5, Appl
22	727.6	21.5	1894	16	US-10-260-937-13	Sequence 229, Appl
23	727.6	21.5	2554	9	US-09-962-832-229	Sequence 1, Appl
24	727.6	21.5	2554	10	US-09-953-067A-1	Sequence 263, Appl
25	727.6	21.5	2554	15	US-10-097-340-263	Sequence 167, Appl
26	727.6	21.5	5049	14	US-09-971-392-167	Sequence 327, Appl
27	727.6	21.5	5049	14	US-10-044-090-327	Sequence 327, Appl
28	724.4	21.4	1894	16	US-10-260-937-10	Sequence 11, Appl
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30	713	21.1	2757	10	US-09-953-067A-5	Sequence 1, Appl
31	705.2	20.8	1902	16	US-10-260-937-1	Sequence 1, Appl
32	705.2	20.8	2706	16	US-10-260-937-3	Sequence 15, Appl
33	703.6	20.8	1899	9	US-09-919-060-15	Sequence 16, Appl
34	703.6	20.8	1899	9	US-09-919-060-16	Sequence 12, Appl
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36	703.6	20.8	2693	9	US-09-919-060-14	Sequence 57, Appl
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38	689.6	20.4	2682	16	US-10-260-937-57	Sequence 9708, Appl
39	597.4	17.6	1713	13	US-10-382-248-7	Sequence 168, Appl
40	552.8	16.3	574	15	US-10-029-386-9708	Sequence 21077, A
41	552	15.4	2329	16	US-09-971-392-168	Sequence 1, Appl
42	523.2	15.4	1746	10	US-10-260-937-12	Sequence 3, Appl
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45	422.6	12.5	542	9	US-09-919-060-3	

ALIGNMENTS

RESULT 1
US-10-191-997-87
Sequence 87, Application US/10191997
Publication No. US20030207834A1
GENERAL INFORMATION:
APPLICANT: Oligos Etc., Inc.
APPLICANT: DALE, Roderic M. K.
APPLICANT: ARROW, Amy
APPLICANT: THOMPSON, Terry
TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
FILE REFERENCE: 54800-5019
CURRENT APPLICATION NUMBER: US/10/191,997
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,820
PRIOR FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn version 3.1
SEQ ID NO 87
LENGTH: 3387
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Cox2: Acc. No. US20030207834A1 M90100
US-10-191-997-87

Query Match 99.8%; Score 3379; DB 16; Length 3387;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY	181	CCAGAGGTATGTATAGATGTTGGATTTCACAGATATAAGTGCATGTATACCGGACAG	240
Db	181	CCAGAGGTATGTATAGATGTTGGATTTCAGATATTAAGTGCATGTATACCGGACAG	240
QY	241	ATTCTATGAGAAAATCTGCTCAACCCGAAATTTTGAACAAGATAAATTTATTTCTGAA	300
Db	241	ATTCTATGAGAAAATCTGCTCAACCCGAAATTTTGAACAAGATAAATTTATTTCTGAA	300
QY	301	ACCACATCCCAACACAGTGCATCATACTTACCACCTTCAAGGGATTTTGGACGTTGT	360
Db	301	ACCACATCCCAACACAGTGCATCATACTTACCACCTTCAAGGGATTTTGGACGTTGT	360
QY	361	GAATACATTCCTCTCTTGAAATGCAATATGATGTATGTGTACATCCAGATCACA	420
Db	361	GAATACATTCCTCTCTTGAAATGCAATATGATGTATGTGTACATCCAGATCACA	420
QY	421	TTTGATTTGACAGTCCACCACTTAACAATGTGACTATATGTGCTACAAAGCTGGAAACCTT	480
Db	421	TTTGATTTGACAGTCCACCACTTAACAATGTGACTATATGTGCTACAAAGCTGGAAACCTT	480
QY	481	CTCTAACCTCTCCTATTATACTAGAGCCCTCTCTGTGCTGATGATGCCCCGACTCC	540
Db	481	CTCTAACCTCTCCTATTATACTAGAGCCCTCTCTGTGCTGATGATGCCCCGACTCC	540
QY	541	CTTGGGGTGTCAAAGGTAAAAAGCAGCTTCTGATTCAAATGAAATGTGGAAAATTTGCT	600
Db	541	CTTGGGGTGTCAAAGGTAAAAAGCAGCTTCTGATTCAAATGAAATGTGGAAAATTTGCT	600
QY	601	TCTTAAGAAAGAAAGTCACTCCCTGATCCCAAGGCTCAACATGATGTTTGCACTTCCTTTC	660
Db	601	TCTTAAGAAAGAAAGTCACTCCCTGATCCCAAGGCTCAACATGATGTTTGCACTTCCTTTC	660
QY	661	CCAGACTTTCACGCAACCACTTTTTCAGACAGATCATTAACGAGGGGCAGCTTTCACCAA	720
Db	661	CCAGACTTTCACGCAACCACTTTTTCAGACAGATCATTAACGAGGGGCAGCTTTCACCAA	720
QY	721	CGGGCTGGGGCATGGGGTGGACTTAATTCATATTTACGGTGAACAATCTGCTGACAGACG	780
Db	721	CGGGCTGGGGCATGGGGTGGACTTAATTCATATTTACGGTGAACAATCTGCTGACAGACG	780
QY	781	TAAACTGCGCTTTTTCAGAGTGGAAAAATGAAATATCAGATATATGATGAGAGATGTA	840
Db	781	TAAACTGCGCTTTTTCAGAGTGGAAAAATGAAATATCAGATATATGATGAGAGATGTA	840
QY	841	TTCCTCCCACTCAAAAGATCTCAGAGGACAGATGATCTACCCCTCTCTCAAGTCCCTGACGA	900
Db	841	TTCCTCCCACTCAAAAGATCTCAGAGGACAGATGATCTACCCCTCTCTCAAGTCCCTGACGA	900
QY	901	TCTACGTTTGTGTGTGGGGCAGAGGTCTTGTGTGTGGTCTGGTCTGTGATGTATGC	960
Db	901	TCTACGTTTGTGTGTGGGGCAGAGGTCTTGTGTGTGGTCTGGTCTGTGATGTATGC	960
QY	961	CACAAATCTGGCTGGGGGAACAACAAGAGTATGTGATGTCTTAAACAGAGACATCTCTGA	1020
Db	961	CACAAATCTGGCTGGGGGAACAACAAGAGTATGTGATGTCTTAAACAGAGACATCTCTGA	1020
QY	1021	ATGGGGTATGAGCAGTGTCTCAGACACAGCAGGCTATATCTGATGAGAGACATATTAA	1080
Db	1021	ATGGGGTATGAGCAGTGTCTCAGACACAGCAGGCTATATCTGATGAGAGACATATTAA	1080
QY	1081	GATTGTGATGAAGATTAATGTGCAACATTTGATGTGCTATCATCTTCAACCTGAAATTTGA	1140
Db	1081	GATTGTGATGAAGATTAATGTGCAACATTTGATGTGCTATCATCTTCAACCTGAAATTTGA	1140
QY	1141	CCCAACAATCACTTTTCAACAAACATTCACAGTACCAAAATCGTATGCTGCTGAATTTAA	1200
Db	1141	CCCAACAATCACTTTTCAACAAACATTCACAGTACCAAAATCGTATGCTGCTGAATTTAA	1200

QY	1201	CACCCCTATCACTGGCATCCCTCTTGCCCTGCACACCTTTCAAAATTCATGACCGAATAA	1260
Db	1201	CACCCCTATCACTGGCATCCCTCTTGCCCTGCACACCTTTCAAAATTCATGACCGAATAA	1260
QY	1261	CAACTATCAAGTTATCTCAACAACCTATATTTGCTGGACAACGGAATTAACCAAGTT	1320
Db	1261	CAACTATCAAGTTATCTCAACAACCTATATTTGCTGGACAACGGAATTAACCAAGTT	1320
QY	1321	TGTTGAATCATTTCAACGAGCAAAATTTGCTGGACGGGTGTGCTGGTGGAGATGTTCCACC	1380
Db	1321	TGTTGAATCATTTCAACGAGCAAAATTTGCTGGACGGGTGTGCTGGTGGAGATGTTCCACC	1380
QY	1381	CGCAGTACAGAAAGTATATACAGAGCTTCATTTACACAGACAGGACAGATGAATTAACAGTC	1440
Db	1381	CGCAGTACAGAAAGTATATACAGAGCTTCATTTACACAGACAGGACAGATGAATTAACAGTC	1440
QY	1441	TTTTATATAGTACCGCAACGCTTTATGTGTGAAGCCCTTATGAATCATTTTGAAGAACTTATC	1500
Db	1441	TTTTATATAGTACCGCAACGCTTTATGTGTGAAGCCCTTATGAATCATTTTGAAGAACTTATC	1500
QY	1501	AGGAGAAAAGGAAATGTCTGCAGAGTTGGAAACACTTATGTGATCATGATGCTGTGGA	1560
Db	1501	AGGAGAAAAGGAAATGTCTGCAGAGTTGGAAACACTTATGTGATCATGATGCTGTGGA	1560
QY	1561	GCTGTATCCTGCCCTTTCTGTGTGAAGAAAGCTCTGGCCAGATGCCATCTTTGTGAAGAACAT	1620
Db	1561	GCTGTATCCTGCCCTTTCTGTGTGAAGAAAGCTCTGGCCAGATGCCATCTTTGTGTGAAGAACAT	1620
QY	1621	GGTATAGTTGGAGACCATCTCTCTGTGAAGAGACTTATAGGTAATGTTATATGTTCTCC	1680
Db	1621	GGTATAGTTGGAGACCATCTCTCTGTGAAGAGACTTATAGGTAATGTTATATGTTCTCC	1680
QY	1681	TGCCCTACTGGAAAGCAAGACCTTTGTGTGAAGAGTGGGTTTCAATCATCAACACTGC	1740
Db	1681	TGCCCTACTGGAAAGCAAGACCTTTGTGTGAAGAGTGGGTTTCAATCATCAACACTGC	1740
QY	1741	CTCAATTCAGTCTCTCATCTGCATATAGAGTGAAGGCTGTCCCTTATCACTCACTTCAGTGT	1800
Db	1741	CTCAATTCAGTCTCTCATCTGCATATAGAGTGAAGGCTGTCCCTTATCACTTCAGTGT	1800
QY	1801	TCCAGATCCAGAGCTCATTTAAAGACGTACCAATCANGACAAGTTCTTCCGCTCCGGACT	1860
Db	1801	TCCAGATCCAGAGCTCATTTAAAGACGTACCAATCANGACAAGTTCTTCCGCTCCGGACT	1860
QY	1861	AGATGATATCAATCCACAGTACTACTMAAAGACGGTGCATGAACTGTAGAAGTCTAA	1920
Db	1861	AGATGATATCAATCCACAGTACTACTMAAAGACGGTGCATGAACTGTAGAAGTCTAA	1920
QY	1921	TGATCATATTTATTTATTTATATAGAACATGTCTATTAATTTATTTATTAATTAATTT	1980
Db	1921	TGATCATATTTATTTATTTATATAGAACATGTCTATTAATTTATTTATTAATTAATTT	1980
QY	1981	AATTTAACTCCCTATAGTTACTTAAACATCTTCTGTAAACAGAAAGTCACTCCCTGTGGC	2040
Db	1981	AATTTAACTCCCTATAGTTACTTAAACATCTTCTGTAAACAGAAAGTCACTCCCTGTGGC	2040
QY	2041	GAGAAAGGAGTCACTTGTGAAGACTTTATGTCACTACTTAAGAATTTGTCTGTGC	2100
Db	2041	GAGAAAGGAGTCACTTGTGAAGACTTTATGTCACTACTTAAGAATTTGTCTGTGC	2100
QY	2101	TGTTAAGTTTGAAGAAACAGTTTTATTTCTGTGTTTTATTAACCAAGAGAAATGAATTTGA	2160
Db	2101	TGTTAAGTTTGAAGAAACAGTTTTATTTCTGTGTTTTATTAACCAAGAGAAATGAATTTGA	2160
QY	2161	CGTCTTTTAACTTGAAATTTCAACTTATATTAATAGAGCGAAAGTAAGATGTTGAATAC	2220
Db	2161	CGTCTTTTAACTTGAAATTTCAACTTATATTAATAGAGCGAAAGTAAGATGTTGAATAC	2220
QY	2221	TTTAAACACTATCAAGAGTCCAAATAGTGAAGATTTTCACTGTGATGATTTTCCAT	2280
Db	2221	TTTAAACACTATCAAGAGTCCAAATAGTGAAGATTTTCACTGTGATGATTTTCCAT	2280
QY	2281	GCATCTTCCATGATGACTTGAAGTAACTATGTTTGAATTTTAAAGTACTTTTGGGTA	2340

Db 481 CTCGACCTCTCTATTATCTAGAGCCCTTCTCTGTCCTGATGATTTGCCGACTCC 540
QY 541 CTGGGGTGTCAAAAGTAAAGACAGCTTCTGATTCAAATGAGATTTGGAAAATTTGCT 600
Db 541 CTGGGGTGTCAAAAGTAAAGACAGCTTCTGATTCAAATGAGATTTGGAAAATTTGCT 600
QY 601 TCTAAGAAAGAAAGTTCAATCCCTGATCCCGAGGCTCAACATGATGTTTGTATTTCTTTC 660
Db 601 TCTAAGAAAGAAAGTTCAATCCCTGATCCCGAGGCTCAACATGATGTTTGTATTTCTTTC 660
QY 661 CCAGCAGCTTCAAGCAGAGTTTTCAGAGCAGATCATAGAGAGGCGCAGCTTTCACCAA 720
Db 661 CCAGCAGCTTCAAGCAGAGTTTTCAGAGCAGATCATAGAGAGGCGCAGCTTTCACCAA 720
QY 721 CGGGCTGGGCGATGGGGGTGGAATTAAATCATATTTTACGGTGAACCTGCTAGACAGCG 780
Db 721 CGGGCTGGGCGATGGGGGTGGAATTAAATCATATTTTACGGTGAACCTGCTAGACAGCG 780
QY 781 TAAACGCGCTTTTCAAGGATGGAATAATGAAATATCAAGTAAATTTGATGAGAGATGTA 840
Db 781 TAAACGCGCTTTTCAAGGATGGAATAATGAAATATCAAGTAAATTTGATGAGAGATGTA 840
QY 841 TCCGCCACAGCTCAAAAGTATCTCAGGCGAGATGATCTACCTCCTCAAGTCCCTGAGCA 900
Db 841 TCCGCCACAGCTCAAAAGTATCTCAGGCGAGATGATCTACCTCCTCAAGTCCCTGAGCA 900
QY 901 TCTACGGTTTCTGTGGGGGAGAGGCTTTGTGTGGTGGCTGGTCTGATGATGATGTC 960
Db 901 TCTACGGTTTCTGTGGGGGAGAGGCTTTGTGTGGTGGCTGGTCTGATGATGATGTC 960
QY 961 CACAAATCTGCGCGGGAACAACAAGATGATGATGATGATGATGATGATGATGATGATG 1020
Db 961 CACAAATCTGCGCGGGAACAACAAGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1021 ATGGGGTATGAGAGTGTTCACAGACAGGCTTAATATCTGATGAGAGAGACTATTA 1080
Db 1021 ATGGGGTATGAGAGTGTTCACAGACAGGCTTAATATCTGATGAGAGAGACTATTA 1080
QY 1081 GATTGTGATGAAATATATGTCACAACACTTGAATGAGTATCACTTCAAACTGAAATTTGA 1140
Db 1081 GATTGTGATGAAATATATGTCACAACACTTGAATGAGTATCACTTCAAACTGAAATTTGA 1140
QY 1141 CCCAAGATCTATTTTCAACAAACATTTCCAGTACCAAAATGATGATGATGATGATGAT 1200
Db 1141 CCCAAGATCTATTTTCAACAAACATTTCCAGTACCAAAATGATGATGATGATGATGAT 1200
QY 1201 CACCTCTATCACTGGCATCCCTCTGTGCTGACACTTTTCAATTCATGACCAAAATA 1260
Db 1201 CACCTCTATCACTGGCATCCCTCTGTGCTGACACTTTTCAATTCATGACCAAAATA 1260
QY 1261 CAACATCAACAGTTTATCTACAAACAATCTATATTTGCTGGAACATGAAATTAACCA 1320
Db 1261 CAACATCAACAGTTTATCTACAAACAATCTATATTTGCTGGAACATGAAATTAACCA 1320
QY 1321 TGTGTAATCATCTACAGGCAAAATGCTGGGAGGCTGCTGGTGAAGGATGTTCCACC 1380
Db 1321 TGTGTAATCATCTACAGGCAAAATGCTGGGAGGCTGCTGGTGAAGGATGTTCCACC 1380
QY 1381 GCGAGTACAGAAAGTATCAGAGGCTTCAATGACAGAGCAGAGCAGATGAAATTAACAG 1440
Db 1381 GCGAGTACAGAAAGTATCAGAGGCTTCAATGACAGAGCAGAGCAGATGAAATTAACAG 1440
QY 1441 TTTTAAATGAGTACCGCAAAAGCTTTATGCTGAAGCCCTATGAAATCAATTTGAAGAA 1500
Db 1441 TTTTAAATGAGTACCGCAAAAGCTTTATGCTGAAGCCCTATGAAATCAATTTGAAGAA 1500
QY 1501 AAGAGAAAGAAAGTATCTGAGAGGTTGGAAGCCTATGAGGATGATGATGATGATGAT 1560
Db 1501 AAGAGAAAGAAAGTATCTGAGAGGTTGGAAGCCTATGAGGATGATGATGATGATGAT 1560
QY 1561 GCTGTATCTGCTCTGTGATGAAAGCTGCGGCGAGATGCGATCTTTGGTGAAGCAAT 1620
Db 1561 GCTGTATCTGCTCTGTGATGAAAGCTGCGGCGAGATGCGATCTTTGGTGAAGCAAT 1620

QY 1621 GGTAGAAAGTTGAGACCAATTTCTTTGAAGAGCTTAAAGGATATGATGATGATGATGAT 1680
Db 1621 GGTAGAAAGTTGAGACCAATTTCTTTGAAGAGCTTAAAGGATATGATGATGATGATGAT 1680
QY 1681 TGCCCTACTGAGAGCAAGCACTTTTGGTGAAGAGTGGTGTTCCTTCAATTCATCACTGTC 1740
Db 1681 TGCCCTACTGAGAGCAAGCACTTTTGGTGAAGAGTGGTGTTCCTTCAATTCATCACTGTC 1740
QY 1741 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGTCCCTTACTTCAATTCAGTGT 1800
Db 1741 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGTCCCTTACTTCAATTCAGTGT 1800
QY 1801 TCCGATCCAGAGCTCAATTAAGCAAGTCAATCAATGCAAGTCTCCCGCTCCGAGCT 1860
Db 1801 TCCGATCCAGAGCTCAATTAAGCAAGTCAATCAATGCAAGTCTCCCGCTCCGAGCT 1860
QY 1861 AGATGATATCAATCCACAGTACTAATAAGAGCGTGCATGAGCTGATGAAGTCTAA 1920
Db 1861 AGATGATATCAATCCACAGTACTAATAAGAGCGTGCATGAGCTGATGAAGTCTAA 1920
QY 1921 TGATCATATTTATTTATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 1921 TGATCATATTTATTTATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
QY 1981 ATATTAAGCTCTATGATTTAATCAATCTTGTAAAGAGTCAAGTCACTGCTGTCG 2040
Db 1981 ATATTAAGCTCTATGATTTAATCAATCTTGTAAAGAGTCAAGTCACTGCTGTCG 2040
QY 2041 GAGAAAGAGTCAATCTGTGAGAGACTTTATGTCATCACTCTAAGATTTTGTCTGTCG 2100
Db 2041 GAGAAAGAGTCAATCTGTGAGAGACTTTATGTCATCACTCTAAGATTTTGTCTGTCG 2100
QY 2101 TGTAAAGTTTGAAGAAAGCTTTTATCTGTGTTTAAACAGAGAGAAAGAGTTTGA 2160
Db 2101 TGTAAAGTTTGAAGAAAGCTTTTATCTGTGTTTAAACAGAGAGAAAGAGTTTGA 2160
QY 2161 GGTCTTTTAACTTGAATTTCACTTAATTAAGAGAGAAAGATGTTGAATAC 2220
Db 2161 GGTCTTTTAACTTGAATTTCACTTAATTAAGAGAGAAAGATGTTGAATAC 2220
QY 2221 TTAACACTATCAAGATGAGCAAAATGCTGAAGTTTAACTGCTGATGATTTCAAT 2280
Db 2221 TTAACACTATCAAGATGAGCAAAATGCTGAAGTTTAACTGCTGATGATTTCAAT 2280
QY 2281 GCATCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
Db 2281 GCATCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
QY 2341 TTTTCTGTCAACAAAGAGGATCACTGATCAATTAATGAAATTTGAATTTGA 2400
Db 2341 TTTTCTGTCAACAAAGAGGATCACTGATCAATTAATGAAATTTGAATTTGA 2400
QY 2401 CATTAACAGTAAATTTCACTGATTTTAAATCAAGATGAAATTAATTTGAATTTGA 2460
Db 2401 CATTAACAGTAAATTTCACTGATTTTAAATCAAGATGAAATTAATTTGAATTTGA 2460
QY 2461 TCTAAATTCATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Db 2461 TCTAAATTCATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
QY 2521 CTGTGATATATCAAAAGAGGCTGTGATGATTTAAATCTGTAATCAATGATGAAAT 2580
Db 2521 CTGTGATATATCAAAAGAGGCTGTGATGATTTAAATCTGTAATCAATGATGAAAT 2580
QY 2581 TTAATCAATTTGCTGTTAAATTTTAAATGATGATGATGATGATGATGATGATGAT 2640
Db 2581 TTAATCAATTTGCTGTTAAATTTTAAATGATGATGATGATGATGATGATGATGAT 2640
QY 2641 AACCTTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700
Db 2641 AACCTTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700

Query Match	95.0%	Score 3216.6	DB 10	Length 4465
Best Local Similarity	97.7%	Pred No. 0		
Matches 3310	Conservative	0	Mismatches 59	Indels 18
				Gaps 4

[illegible]

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Db 1118 GATTGTATGTAAGATATGTCAGCACTTGAAGGCTATCATCTTCAACTGGAATTTGA 1177
Qy 1141 CCCGAACCTACTTTTCAACCAACAATTCAGATCCAAATGATTTGCTGTAATTTAA 1200
Db 1178 CCCGAACCTACTTTTCAACCAACAATTCAGATCCAAATGATTTGCTGTAATTTAA 1237
Qy 1201 CACCTCTATACATGGGCAATCCCCCTTCTGCTGACACCTTTCAANTCTATGCCGAAATA 1260
Db 1238 CACCTCTATACATGGGCAATCCCCCTTCTGCTGACACCTTTCAANTCTATGCCGAAATA 1297
Qy 1261 CAACCTATCAAGTTTATCTCAACAACCTATATTTGCTGGAACATGGAATTTACCAAGTT 1320
Db 1298 CAACCTATCAAGTTTATCTCAACAACCTATATTTGCTGGAACATGGAATTTACCAAGTT 1357
Qy 1321 TGTGAATCATTCACAGGCAAAATTTGCTGCAAGGTTGCTGCTGTAGGAATGTTCAAC 1380
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Qy 1501 AGAGAAAGAAATGCTCTGCAAGAGTTGGAAGCACTTATGCTGACATGATGCTGTGGA 1560
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Db 1598 GCTGATCTGCTGCTCTGCTGTAAGAAAGCTCGGCAATGCAATCTTTGGAAGCAAT 1657
Qy 1621 GGTGAAGTTGGAGCAACCTTCTCCTTGAAAGCACTTATGGGTATGTTATATGTTCTCC 1680
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Qy 1681 TGCTTACTGGAAGCCAGACCTTTTGGTGGAGAGTGGGTTTCAATCATCAACATGCG 1740
Db 1718 TGCTTACTGGAAGCCAGACCTTTTGGTGGAGAGTGGGTTTCAATCATCAACATGCG 1777
Qy 1741 CTCAATTCAGTCTCATCTGCAATTAAGTGAAGGGCTGCCCTTACTCTCAATTCAGT 1800
Db 1778 CTCAATTCAGTCTCATCTGCAATTAAGTGAAGGGCTGCCCTTACTCTCAATTCAGT 1837
Qy 1801 TCCAGATCCAGAGCTCATTTAAACAGTCAACATCAATGCAAGTTCTTCCCGCTCGGACT 1860
Db 1838 TCCAGATCCAGAGCTCATTTAAACAGTCAACATCAATGCAAGTTCTTCCCGCTCGGACT 1897
Qy 1861 AGATGATATCAATCCCAAGTACTCTAATAAGAGAGGTTGCTGAGCACTGTAAGACTTAA 1920
Db 1898 AGATGATATCAATCCCAAGTACTCTAATAAGAGAGGTTGCTGAGCACTGTAAGACTTAA 1957
Qy 1921 TGATGATATTTATTTATTTATTAAGAACATGCTCTATTAATTTATTTATTTATTTATTT 1980
Db 1958 TGATGATATTTATTTATTTATTAAGAACATGCTCTATTAATTTATTTATTTATTTATTT 2017
Qy 1981 ATATTAACTCCTTATGTTACTTAAATCTTCTGTAACAGAGTCAATCTCTGTGGG 2040
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Db 2138 TGTTAGTTTGAAGAAAGCTTTTATCTGTTTATTAACAGAGAGAAATGAGTTTGA 2197
Qy 2161 GCTCTTTTACTTGAATTTCAACTTATATTAAGAGCAAGTAAGATGTTGAATAC 2220
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Qy 2221 TTAAAGCTATACAAATGCCCCAAATGCTGAAGTTTATACNCTGCGATGTTCAAT 2280
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Db 2318 GCATCTTCATGATGATTAAGAGTAACTAATGTTGAAATTTTAAAGTACTTTGGGTA 2377
Qy 2341 TTTTCTGTCAATCAAC-AAAACAGTATCAATGATTAATTAATGAATTTAAATTAAG 2399
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Db 2438 ACATTTACAGTAATTTATGATGCTATCTTTTAAATTCAGCAATGAACATTAATTTGAAT 2497
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Db 2498 TTTTAAATTCATGAGGTAGTAATCACTGTAAAGCTTGTGATTTCTTAAAGTTATTA 2557
Qy 2520 ACTGTACATATCAAAAAGAGCTGTCTTGATTTAAATCTGTAATTAATGATGAAT 2579
Db 2558 ACTGTACATATCAAAAAGAGCTGTCTTGATTTAAATCTGTAATTAATGATGAAT 2617
Qy 2580 TTTTCTCAATGCTGTGTTAAATATTTTATTAAGATGTTCTTTTCAACCAAGATAT 2639
Db 2618 TTTTCTCAATGCTGTGTTAAATATTTTATTAAGATGTTCTTTTCAACCAAGATAT 2677
Qy 2640 AAACCTTTTATGCTGATCTGTTAAACCTCTTTTAAATCAAAATGCCAAATTTATTAAG 2699
Db 2678 AAACCTTTTATGCTGATCTGTTAAACCTCTTTTAAATCAAAATGCCAAATTTATTAAG 2737
Qy 2700 GTGTGAGAGCCACATGCAATGTTATCTCAAAATTAAGATATCTGTTGATATTCAGAA 2759
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Db 2851 TTTAA-----AATAGCAATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2901
Qy 2880 TTTAACTTTTGAAGCAAACTTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2939
Db 2902 GTTTAACTTTTGAAGCAAACTTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2961
Qy 2940 TTTTCTATGAGGTTATGAGTACCAAGCTGTGCTGTAATTAAGATATGTTTCTCAGA 2999
Db 2962 TTTTCTATGAGGTTATGAGTACCAAGCTGTGCTGTAATTAAGATATGTTTCTCAGA 3021
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Db 3022 TTTTCTGTTGATACGTTTATTTAGAGCTCATATCAATTTGCAAAAGTAGCAATGACT 3081
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Qy 3180 TTTTCTCTTTTAAAGCAATTTTGTCTAAGAGACAGCTTTCTCAACATCTTCTCTCT 3239
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Qy 3240 ATTTTCTTTTACTAGTTTAAATCAAGCTTACTTCTGTTGAGATCTGCTGCTGCTGCT 3299
Db 3261 ATTTTCTTTTACTAGTTTAAATCAAGCTTACTTCTGTTGAGATCTGCTGCTGCTGCT 3320
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;; CURRENT FILING DATE: 2002-06-12
;; PRIOR APPLICATION NUMBER: PCT/GB02/01662
;; PRIOR FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: PCT/GB01/05458
;; PRIOR FILING DATE: 2001-12-10
;; NUMBER OF SEQ ID NOS: 549
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 238
;; LENGTH: 4465
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
US-10-170-385-238

Query Match 95.0%; Score 3216.6; DB 13; Length 4465;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 3310; Conservative 0; Mismatches 59; Indels 18; Gaps 4;

QY 1 GTCCAGAACTCCTCAGCAGCGCTCCTTCAGCTCCACAGCAGCAGCGCCCTCAGACAGA 60
DB 38 GTCCAGAACTCCTCAGCAGCGCTCCTTCAGCTCCACAGCAGCAGCGCCCTCAGACAGA 97
QY 61 AAGCTTACCCCGCGCGCGCGCTCCGCGCGCTGCGATGCTGCGCGCGCGCTGCT 120
DB 98 AAGCTTACCCCGCGCGCGCGCTCCGCGCGCTGCGATGCTGCGCGCGCGCTGCT 157
QY 121 GTGGCGGCTCTGGGCGCTCAGCCATACAGCAATCTCTGCTTCCACCCATGTCAAA 180
DB 158 GTGGCGGCTCTGGGCGCTCAGCCATACAGCAATCTCTGCTTCCACCCATGTCAAA 217
QY 181 CCGAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 218 CCGAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 277
QY 241 ATTCTATGAGAAAACTGCTCAACACCGAATTTTGAAGAATAAATTAATTTCTGAA 300
DB 278 ATTCTATGAGAAAACTGCTCAACACCGAATTTTGAAGAATAAATTAATTTCTGAA 337
QY 301 ACCGACTCCAAACAGTGCATCATCTTACCACTTCAAGGATTTTGAACGTTGT 360
DB 338 ACCGACTCCAAACAGTGCATCATCTTACCACTTCAAGGATTTTGAACGTTGT 397
QY 361 GAATTAACATTCCTCTCTGGAATGGAATGATGATGATGATGATGATGATGATGATGAT 420
DB 398 GAATTAACATTCCTCTCTGGAATGGAATGATGATGATGATGATGATGATGATGATGAT 457
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DB 458 TTGATGACAGTCCACCACTTAACATGCTGATGCTGCTCAAAAGCTGGAGGCTT 517
QY 481 CTCTAACCTCTCTATTTATCTAGAGCCCTTCTCTGCTGATGATGATGATGATGATGAT 540
DB 518 CTCTAACCTCTCTATTTATCTAGAGCCCTTCTCTGCTGATGATGATGATGATGATGAT 577
QY 541 CTGGGATGTCAGAAAGTAAAGAGAGCTCTGATTTCAATGAAATGATGATGATGATGAT 600
DB 578 CTGGGATGTCAGAAAGTAAAGAGAGCTCTGATTTCAATGAAATGATGATGATGATGAT 637
QY 601 TCTAAGAGAAAGTCAATCCCTGATCCCAAGGCTCAAAATGATGATGATGATGATGAT 660
DB 638 TCTAAGAGAAAGTCAATCCCTGATCCCAAGGCTCAAAATGATGATGATGATGATGAT 697
QY 661 CCAGCACTTCAAGCAGCAGTTTTCAGAGATCATTAAGCGAGGCGCAGCTTTCACCA 720
DB 698 CCAGCACTTCAAGCAGCAGTTTTCAGAGATCATTAAGCGAGGCGCAGCTTTCACCA 757
QY 721 CCGGCTGGGCGCATGGGGTGAATTAATGATATTTAAGGAACTCTGGCTGAGAGAGG 780
DB 758 CCGGCTGGGCGCATGGGGTGAATTAATGATATTTAAGGAACTCTGGCTGAGAGAGG 817
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DB 818 TAAACTGGCGCTTTTCAAGGATGAAAAATGAATATCAGATTAATGATGAGAGATGTA 877

QY 841 TCTTCCCAAGTCAAGATTAATCAGCAGAGATGATCTAACCTCTCAAGTCCCTGAGCA 900
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DB 1058 ATGGGATGATGAGAGAGTGTCCAGACAGAGGCTAATCTGATGAGAGAGATGATGAT 1117
QY 1081 GATTGTGATGAGATTAATGAGCAACTTGAATGAGCTGATCACTCAAACTGAATTTGA 1140
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DB 1178 CCGAGAACTATTTTCAACAAACAAATTCAGTACCAAAATGATGATGATGATGATGAT 1237
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DB 1238 CACCCTCATCACTGGGATCCCTCTGCGCTGACACCTTCAATTCATGACAGAAATA 1297
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DB 1358 TGTGATCAATTCACAGGCAATGCTGCGAGGCTTGTGATGATGATGATGATGATGAT 1417
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DB 1478 TTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1537
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DB 1778 CTCATATCAGTCTCTCATCTGCAATTAAGGAGAGGCTGCTTACTTCACTCATGATG 1837
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QY 1921 TGATCATATTTATTTATTTATGAAACCATGCTATTAATTTAATTTAATTTATTT 1980

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Db	278	ATTCTATGGAGAAA	CTGCTCAAC	CCGGAA	TTTTTGAC	AAATTA	TTTCTGAA	337
QY	301	ACCCACTCCAAA	CAGAGTSC	ACTAC	TACTTAC	CCCACTT	CAAGGGATTTT	360
Db	338	ACCCACTCCAAA	CAGAGTSC	ACTAC	TACTTAC	CCCACTT	CAAGGGATTTT	397
QY	361	GAATTAAC	TTCCCTCTT	CGAAATG	CAATTATG	ATGATG	TGAGATCCAGATCA	420
Db	398	GAATTAAC	TTCCCTCTT	CGAAATG	CAATTATG	ATGATG	TGAGATCCAGATCA	457
QY	421	TTGATGAC	AGTCCACCA	CTTA	CAATGCT	ACTATG	CTTCAAAAAGCTGGAA	480
Db	458	TTGATGAC	AGTCCACCA	CTTA	CAATGCT	ACTATG	CTTCAAAAAGCTGGAA	517
QY	481	CTTAACCT	CTCTTA	TTATTA	CTAGAG	CCCTT	CTCTGCTGATGATG	540
Db	518	CTTAACCT	CTCTTA	TTATTA	CTAGAG	CCCTT	CTCTGCTGATGATG	577
QY	541	CTTGGGTGT	CAAAAGT	TAATAA	AGAGCTT	CTGATTA	CAATGAGATTTG	600
Db	578	CTTGGGTGT	CAAAAGT	TAATAA	AGAGCTT	CTGATTA	CAATGAGATTTG	637
QY	601	TCTAAGA	GAAGTTC	ATCCCTG	ATCCAG	GGCTCAAA	CTGATGTTG	660
Db	638	TCTAAGA	GAAGTTC	ATCCCTG	ATCCAG	GGCTCAAA	CTGATGTTG	697
QY	661	CCAGCACTT	CAAGCAG	CCAGT	TTTCAAG	AGATCA	TAAGGAGGGCCAGCTT	720
Db	698	CCAGCACTT	CAAGCAG	CCAGT	TTTCAAG	AGATCA	TAAGGAGGGCCAGCTT	757
QY	721	CGGGCTGG	GCATG	GGGTGA	CTTAAT	TCATATTTA	CGGTGAACTCTG	780
Db	758	CGGGCTGG	GCATG	GGGTGA	CTTAAT	TCATATTTA	CGGTGAACTCTG	817
QY	781	TAAATCG	CGCTTTT	CAAGATG	GAATAA	TATCAG	TAAATTG	840
Db	818	TAAATCG	CGCTTTT	CAAGATG	GAATAA	TATCAG	TAAATTG	877
QY	841	TCCCTCC	CAAGTCA	AAATAT	CTCAG	AGATG	ATCCTCAAGCTT	900
Db	878	TCCCTCC	CAAGTCA	AAATAT	CTCAG	AGATG	ATCCTCAAGCTT	937
QY	901	TCTA	CGGTG	CTGCTG	GGGAG	AGATCTT	GTGATGCTGATG	960
Db	938	TCTA	CGGTG	CTGCTG	GGGAG	AGATCTT	GTGATGCTGATG	997
QY	961	CACAAT	CTGGCTG	CGGGA	CAACA	CAGATG	ATGATGCTTAA	1020
Db	998	CACAAT	CTGGCTG	CGGGA	CAACA	CAGATG	ATGATGCTTAA	1057
QY	1021	ATGGGGT	GATGAC	AGTGT	TTCCAG	ACAGGCTT	ATATCTGATGGA	1080
Db	1058	ATGGGGT	GATGAC	AGTGT	TTCCAG	ACAGGCTT	ATATCTGATGGA	1117
QY	1081	GATTGAT	GATTGA	ATGATG	CAACA	CTTGA	TGATGCTTAA	1140
Db	1118	GATTGAT	GATTGA	ATGATG	CAACA	CTTGA	TGATGCTTAA	1177
QY	1141	CCGAGA	ACTATCTT	TTCAA	CAAAAG	ATTCAG	TACCAAAATG	1200
Db	1178	CCGAGA	ACTATCTT	TTCAA	CAAAAG	ATTCAG	TACCAAAATG	1237
QY	1201	CACCTCT	ATCACTG	GCATC	CCCTT	CTGCTG	ACACCTTCA	1260
Db	1238	CACCTCT	ATCACTG	GCATC	CCCTT	CTGCTG	ACACCTTCA	1297
QY	1261	CAACTTA	CAACAG	TTATTTA	CAACA	CTCTAT	TATGCTGGA	1320
Db	1298	CAACTTA	CAACAG	TTATTTA	CAACA	CTCTAT	TATGCTGGA	1357
QY	1321	TGTTGA	TCAATC	ATC	CAAGCA	AAATTTG	CTGGCAGG	1380
Db	1358	TGTTGA	TCAATC	ATC	CAAGCA	AAATTTG	CTGGCAGG	1417
QY	1381	CGCAGT	ACAGAA	AGTAT	CAACAG	CTTCA	TTGACCA	1440
Db	1418	CGCAGT	ACAGAA	AGTAT	CAACAG	CTTCA	TTGACCA	1477
QY	1441	TTTTA	TGAGTA	ACGCA	AAAGCTT	TATGCT	GAAGCCCTATG	1500
Db	1478	TTTTA	TGAGTA	ACGCA	AAAGCTT	TATGCT	GAAGCCCTATG	1537
QY	1501	AGGAGAA	AGTGA	AAATG	CTG	CAGATG	GAAGCACTA	1560
Db	1538	AGGAGAA	AGTGA	AAATG	CTG	CAGATG	GAAGCACTA	1597
QY	1561	GCTGAT	CTCCTG	CTTCTG	TGAGAA	AAAGCTT	CGGCAGATG	1620
Db	1598	GCTGAT	CTCCTG	CTTCTG	TGAGAA	AAAGCTT	CGGCAGATG	1657
QY	1621	GGTGA	AGTGGAG	ACACAT	CTCCTG	GAAGCACTA	TGAGTATG	1680
Db	1658	GGTGA	AGTGGAG	ACACAT	CTCCTG	GAAGCACTA	TGAGTATG	1717
QY	1681	TGCTTA	CTGGA	AGC	CAAGCA	CTTTT	TGATGAGAGT	1740
Db	1718	TGCTTA	CTGGA	AGC	CAAGCA	CTTTT	TGATGAGAGT	1777
QY	1741	CTCAAT	CACTCT	CTCA	CTG	CAATTA	CACTCTCT	1800
Db	1778	CTCAAT	CACTCT	CTCA	CTG	CAATTA	CACTCTCT	1837
QY	1801	TCCAG	ATCCAG	AGTCA	TTTAA	AAAGAG	CGGTGATG	1860
Db	1838	TCCAG	ATCCAG	AGTCA	TTTAA	AAAGAG	CGGTGATG	1897
QY	1861	AGATGA	TATAT	ATCC	CACTA	CTA	TAAGAA	1920
Db	1898	AGATGA	TATAT	ATCC	CACTA	CTA	TAAGAA	1957
QY	1921	TGAT	CATATTT	ATTTAT	TATG	AAACAT	GTCTATTA	1980
Db	1958	TGAT	CATATTT	ATTTAT	TATG	AAACAT	GTCTATTA	2017
QY	1981	ATATTA	ACCTT	ATGCTT	TAACAT	CTTCTG	TAAACA	2040
Db	2018	ATATTA	ACCTT	ATGCTT	TAACAT	CTTCTG	TAAACA	2077
QY	2041	GAGAA	AGAGT	CACTA	CTTGA	AGACCTT	TATGCTG	2100
Db	2078	GAGAA	AGAGT	CACTA	CTTGA	AGACCTT	TATGCTG	2137
QY	2101	TGTTA	AGTTG	GA	AAACAG	TTTAT	CTGTTAT	2160
Db	2138	TGTTA	AGTTG	GA	AAACAG	TTTAT	CTGTTAT	2197
QY	2161	CGTCTT	TATTA	CTGA	TTTCA	CTTAT	TATTA	2220
Db	2198	CGTCTT	TATTA	CTGA	TTTCA	CTTAT	TATTA	2257
QY	2221	TAAAC	ACTAT	CA	AGATG	CCAAATG	CTGAAAGT	2280
Db	2258	TAAAC	ACTAT	CA	AGATG	CCAAATG	CTGAAAGT	2317
QY	2281	GATCTT	CA	TGATG	AAAGT	TA	CTGAAAT	2340
Db	2318	GATCTT	CA	TGATG	AAAGT	TA	CTGAAAT	2377
QY	2341	TTTTT	CTG	CA	CAAA	AAAGCTT	CAAGCTT	2399
Db	2378	TTTTT	CTG	CA	CAAA	AAAGCTT	CAAGCTT	2437
QY	2400	ACATTA	CA	AGTAA	TTTCA	TGCTA	CTTTTAA	2459


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Db 398 GAAATAACATTCCTCTTCCGAAATGCAATTAATGAGTAATGCTTGAACATCCAGATCACAA 457
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Qy 481 CTCTAACCTCTCTTATTAATGAGAGCTTCTCTGCTGATGATGATGCTCCGACATCC 540
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Qy 541 CTGGGATGCAAAAGGTAATAAGACCTTCTGATCAATGAGATGAGTGGAAAAATTTGCT 600
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Qy 601 TCTAAGAAAGAAAGTTCAATCCCTGATCCCAAGGCTCAAAACATGATGTTGCAATCTTTGCG 660
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QY 2460 TTTTAAATTCATAGGGTATGATCACTGTAATCACTGTTGATTTCTTAAAGTTATTA 2519
Db 2498 TTTTAAATTCATAGGGTATGATCACTGTAATCACTGTTGATTTCTTAAAGTTATTA 2557
QY 2520 ACTGTACATATACCAAAAGAGCTGCTGGAATTTAAATCTGTAATCAGATGAAT 2579
Db 2558 ACTGTACATATACCAAAAGAGCTGCTGGAATTTAAATCTGTAATCAGATGAAT 2617
QY 2580 TTTTCTACATTTGCTGTTAAATATTTTATAGTATGTTCTTTTACCAAGAGTAT 2639
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QY 2880 TTTTAACTTTTGAAGCAACTTTTATAGCCTTGTCAGTCCAGACTGTACTGAGA 2939
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QY 3240 ATTTTGTTTTATCTATGTTTAAAGTACAGATTTCTTCTTGAAGTCTGCTATATTTTC 3299
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DB 3351 CTTAAGAAATTTAAAAAAGAAAAA 3377

RESULT 10
US-10-071-766-46
; Sequence 46, Application US/10071766
; Publication No. US20020192678A1
; GENERAL INFORMATION:
; APPLICANT: Huel-Mei Chen
; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE
; FILE REFERENCE: PA-0043 US
; CURRENT APPLICATION NUMBER: US/10/071,766
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PERL Program
; SEQ ID NO 46
; LENGTH: 4496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020192678A1 271804.3
US-10-071-766-46

Query Match 94.9%; Score 3215; DB 14; Length 4496;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 3309; Conservative 0; Mismatches 60; Indels 18; Gaps 4;

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OY 61 AAGCTTACCCCGCGCGCGCGCTGCGCGCGCTGCGATGCTGCGCGCGCTGCTGCT 120
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OY 121 GTGGCGGCTCTGCGCTCAGCCATACAGCAATCTTGTCTGCCATCCCATGCAAAA 180
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OY 181 CCGAGGTGTATGTATGAGTGTGGATTTGACAGATTAAGTCAGATTTGACCCGAGAG 240
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 RESULT 11
 US-10-247-671-126
 ; Sequence 126, Application US/10247671
 ; Publication No. US20030194721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mikita, Thomas
 ; APPLICANT: Shiffman, Dov
 ; APPLICANT: Porter, Gordon, J.
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
 ; FILE REFERENCE: PA-0050 US
 ; CURRENT APPLICATION NUMBER: US/10/247, 671
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: 60/323,784
 ; PRIOR FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 186
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 126
 ; LENGTH: 4750
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030194721A1 271804.3
 ; US-10-247-671-126
 Query Match 94.9%; Score 3215; DB 15; Length 4750;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 3309; Conservative 0; Mismatches 60; Indels 18; Gaps 4;
 Qy 1 GTCCAGGAATCTCTCAGCAAGCGCTCTCTTCACTCCACAGCAGACCGCCCTCAACAGCA 60
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 Db 421 TTTGATTAAGTCAAGTCAACCAATTAACATGCTGATGCTGATGCTGATGCTGATGCTG 480


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QY 2820 CTGGAACATAAAGCAATACCAAGAGAGAAAGCCCAATATTGTTCCAAATTTAGG 2879
Db 3075 TTTAA-----AATAAGCAATACCAAGAGAGAAAGCCCAATATTGTTCCAAATTTAG 3125
QY 2880 TTTAACTTTTGAAGCAAACTTTTTCCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2939
Db 3126 GTTTAACTTTGGAAGCAAACTTTTTCCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3185
QY 2940 TTTTGCTATGAGTGAATAGAGTACCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2999
Db 3186 TTTTGCTATGAGTGAATAGAGTACCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3245
QY 3000 TTTTCTGTTGACAGTTAATTAGAGTGCATATCAGATTGCAAAAGTACCAATGACCT 3059
Db 3246 TTTTCTGTTGACAGTTAATTAGAGTGCATATCAGATTGCAAAAGTACCAATGACCT 3305
QY 3060 CATAAATATACCTCTCAAAATGCTAAATTCATTTCCATTTTATTTATCTCAGTCTT 3119
Db 3306 CATAAATATACCTCTCAAAATGCTAAATTCATTTCCATTTTATTTATCTCAGTCTT 3365
QY 3120 GAAGCCAAATCAGTAGTGCATTGGAATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 3179
Db 3366 GAAGCCAAATCAGTAGTGCATTGGAATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 3245
QY 3180 TTTTCTCTTTTACGCTTTTGTCTAAGAGACAGCTCTCTCAAACTTGCTGCTCTCT 3239
Db 3426 TTTTCTCTTTTACGCTTTTGTCTAAGAGACAGCTCTCTCTCAAACTTGCTGCTCTCT 3484
QY 3240 ATTTGTTTACTGTTTAAAGATCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3299
Db 3485 ATTTGTTTACTGTTTAAAGATCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3354
QY 3300 TTACCTGAACTTTGCAAGTTTTCAGGTAAACCTCAGCTCAGAGCTGCTATTTAGCTCT 3359
Db 3545 TTACCTGAACTTTGCAAGTTTTCAGGTAAACCTCAGCTCAGAGCTGCTATTTAGCTCT 3604
QY 3360 CTTAAGAGATTTAAAAAATTTAAAAA 3386
Db 3605 CTTAAGAGATTTAAAAAATTTAAAAA 3631

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; NAME/KEY: unsure
; LOCATION: 2551
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-477

Query Match 74.2%; Score 2513.4; DB 14; Length 2563;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2531; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 1 GTCCAGGAACCTCTCAGAGAGGCTCTCTTCAAGCTTCACAGCCAGACGCTCAGACAGA 60
Db 8 GTCCAGGAACCTCTCAGAGAGGCTCTCTTCAAGCTTCACAGCCAGACGCTCAGACAGA 67
QY 61 AAGCTACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 120
Db 68 AAGCTACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 127
QY 121 GTGCGCGGTCTGCGCGCTCAGCCATACAGCAAAATCTGCTGTTCCACCATGTCAAA 180
Db 128 GTGCGCGGTCTGCGCGCTCAGCCATACAGCAAAATCTGCTGTTCCACCATGTCAAA 187
QY 181 CCGAGGTGTATGTATGAGTGTGGATTTGACCAAGTATAGTGCATTTGCGATCCGACAG 240
Db 188 CCGAGGTGTATGTATGAGTGTGGATTTGACCAAGTATAGTGCATTTGCGATCCGACAG 247
QY 241 ATTCTATGAGAAATGCTCAACACCGGAATTTTACAGAAATTAATTTTCTGAA 300
Db 248 ATTCTATGAGAAATGCTCAACACCGGAATTTTACAGAAATTAATTTTCTGAA 307
QY 301 ACCGACTCAAAACAGTGCATACATACCTTCAAGGAAATTTTGAAGCTTGT 360
Db 308 ACCGACTCAAAACAGTGCATACATACCTTCAAGGAAATTTTGAAGCTTGT 367
QY 361 GAATTAATTCCTCTCTCTTGAATGCAATTTATAGTTATGTGTGACATTCAGATACA 420
Db 368 GAATTAATTCCTCTCTCTTGAATGCAATTTATAGTTATGTGTGACATTCAGATACA 427
QY 421 TTGATGAGACAGTCCACCACTTACATATGCTAGTGTGCTAGCAAAAGCTGGGAAGCTT 480
Db 428 TTGATGAGACAGTCCACCACTTACATATGCTAGTGTGCTAGCAAAAGCTGGGAAGCTT 487
QY 481 CTCTAACCTCTCTATTTATCTAGAGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 488 CTCTAACCTCTCTATTTATCTAGAGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTG 547
QY 541 CTGGGCTCAAAAGGTAAAGAGAGCTTCTGATTCAAATGAGATTGTGAAAAATTGCT 600
Db 548 CTGGGCTCAAAAGGTAAAGAGAGCTTCTGATTCAAATGAGATTGTGAAAAATTGCT 607
QY 601 TCTAAGAGAAAGTTCAATCCCTGATCCCGAGGCTCAAAATGATATGTTGCAATCTTTC 660
Db 608 TCTAAGAGAAAGTTCAATCCCTGATCCCGAGGCTCAAAATGATATGTTGCAATCTTTC 667
QY 661 CAGACCTTCAGCAGCAGATTTTCAAGACAGATCAATACGAGGCGCAGCTTTCACCA 720
Db 668 CAGACCTTCAGCAGCAGATTTTCAAGACAGATCAATACGAGGCGCAGCTTTCACCA 727
QY 721 CGGCTGGGCTATGGGCTGAGCTTAAATCAATTTACGTTGAAACTCTGCTGACAGCG 780
Db 728 CGGCTGGGCTATGGGCTGAGCTTAAATCAATTTACGTTGAAACTCTGCTGACAGCG 787
QY 781 TAAACTGCGGCTTTCAAGGATGAAATGAAATTCAGATATTTGATGAGAGAGATGTA 840
Db 788 TAAACTGCGGCTTTCAAGGATGAAATGAAATTCAGATATTTGATGAGAGAGATGTA 847
QY 841 TCTCTCCACAGTCAAAAGATCTCAGCAGAGATGATCTCTCTCAAGTCCCTGAGCA 900
Db 848 TCTCTCCACAGTCAAAAGATCTCAGCAGAGATGATCTCTCTCAAGTCCCTGAGCA 907
QY 901 TCTAGGTTTGTGCTGGGCTAGAGAGTCTTTGATCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 908 TCTAGGTTTGTGCTGGGCTAGAGAGTCTTTGATCTGCTGCTGCTGCTGCTGCTGCTG 967

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RESULT 12
US-10-044-090-477
; Sequence 477, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 477
; LENGTH: 2563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. US20020137081A1 1217831CBI

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US-09-954-456-324

Query Match 51.0%; Score 1727; DB 9; Length 9453;
 Best Local Similarity 96.1%; Pred. No. 0;
 Matches 1818; Conservative 0; Mismatches 55; Indels 18; Gaps 4;

QY 1497 TTACAGAGAGAGAGAGAGATGTCGAGAGTGGAGACCTCTATGGTGAATCATGATGCTG 1556
 DB TCACAGAGAGAGAGAGAGATGTCGAGAGTGGAGACCTCTATGGTGAATCATGATGCTG 6547
 QY 1557 TGGAGACTGATCTCCCTCTCTGGTGAAGAAACCTCCGCGACATGCCATCTTTGGTGA 1616
 DB TGGAGACTGATCTCCCTCTCTGGTGAAGAAACCTCCGCGACATGCCATCTTTGGTGA 6607
 QY 1617 CCATGGTGAAGTGGAGACCATCTCTCTGAGAGAGCTTATGGGTATGTTATATGTT 1676
 DB CCATGGTGAAGTGGAGACCATCTCTCTGAGAGAGCTTATGGGTATGTTATATGTT 6667
 QY 1677 CTCCTGCTTACTGAGAGCCAGCACTTTGGTGAAGAGTGGTCTTCAATCATCAACA 1736
 DB CTCCTGCTTACTGAGAGCCAGCACTTTGGTGAAGAGTGGTCTTCAATCATCAACA 6727
 QY 1737 CTGCTGCTTACTGAGAGCTCTCTCTGATGAGAGAGTGGTCTTCTTACTTATCA 1796
 DB CTGCTGCTTACTGAGAGCTCTCTCTGATGAGAGAGTGGTCTTCTTACTTATCA 6787
 QY 1797 GTGCTTCAGATCCAGAGCTCATTTAAACAGTCCATCATGAGTCTTCCGCTCG 1856
 DB GTGCTTCAGATCCAGAGCTCATTTAAACAGTCCATCATGAGTCTTCCGCTCG 6788
 QY 1857 GACTGATGATATCAATCCACAGTACTTAAAGAAAGCTGCACTGAGTGAAGT 1916
 DB GACTGATGATATCAATCCACAGTACTTAAAGAAAGCTGCACTGAGTGAAGT 6848
 QY 1917 CTAAGATCATATTTATTTATTTATGAGACATCTCTATATTTATTTATTTAT 1976
 DB CTAAGATCATATTTATTTATTTATGAGACATCTCTATATTTATTTATTTAT 6908
 QY 1977 ATTATATTTAAACCTCTATGTTACTTAAACATCTCTGTAACAGAGTCACTGCT 2036
 DB ATTATATTTAAACCTCTATGTTACTTAAACATCTCTGTAACAGAGTCACTGCT 6968
 QY 2037 TGGGAGAGAGAGTCAATCTGTAAGACCTTTATGTCATCTCTAAAGATTTGCTG 2096
 DB TGGGAGAGAGAGTCAATCTGTAAGACCTTTATGTCATCTCTAAAGATTTGCTG 7028
 QY 2097 TTGCTGTTAAGTTGGAGAAACGTTTTATCTGTTTTATTAACAGAGAAATGAGTT 2156
 DB TTGCTGTTAAGTTGGAGAAACGTTTTATCTGTTTTATTAACAGAGAAATGAGTT 7088
 QY 2157 TTGAGCTCTTTTACTGTAATTTCAACTTATATTAAGAGAGAAATGAGTTGA 2216
 DB TTGAGCTCTTTTACTGTAATTTCAACTTATATTAAGAGAGAAATGAGTTGA 7148
 QY 2217 ATACTTAAACACTATCAAGATGCAAAATGCTGAAAGTTTTCACGCTGATGTTTC 2276
 DB ATACTTAAACACTATCAAGATGCAAAATGCTGAAAGTTTTCACGCTGATGTTTC 7208
 QY 2277 CAATGATCTTCCAGATGATGATTAAGAGTAACTATGTTGAATTTTAAAGTACTTTG 2336
 DB CAATGATCTTCCAGATGATGATTAAGAGTAACTATGTTGAATTTTAAAGTACTTTG 7268
 QY 2337 GGTATTTTCTGTCATCAAC-AAAAAGGTATCGATGATTAATTAATTTTAA 2395
 DB GTTATTTTCTGTCATCAACAAAAAGGTATCGATGATTAATTAATTTTAA 7328
 QY 2396 TTAGACATTAACGATTAATTCATGTTTAAATCAGCAATGAAACATATTTG 2455
 DB TTAGACATTAACGATTAATTCATGTTTAAATCAGCAATGAAACATATTTG 7388
 QY 2456 AAATTTCTAAATTCATAGGTGAGATCACTGTAAGAGTCTTGAATTTCTTAAAGTTA 2515
 DB AAATTTCTAAATTCATAGGTGAGATCACTGTAAGAGTCTTGAATTTCTTAAAGTTA 7448

QY 2516 TTAAACCTGTACATATACCAAAAAAGAGCTGCTGATTTAAATCTGTAAATCATGATG 2575
 DB TTAAACCTGTACATATACCAAAAAAGAGCTGCTGATTTAAATCTGTAAATCATGATG 7508
 QY 2576 AAATTTTACTCAATGCTGTTTAAATATTTTATTAAGTATGTTCTTTTTCACCAAGA 2635
 DB AAATTTTACTCAATGCTGTTTAAATATTTTATTAAGTATGTTCTTTTTCACCAAGA 7568
 QY 2636 GTATTAACCTTTTATAGTGTACGTAAACCTTCTTTTAAATGCAAAATTTAT 2695
 DB GTATTAACCTTTTATAGTGTACGTAAACCTTCTTTTAAATGCAAAATTTAT 7628
 QY 2696 TAAAGTGTGAGAGCCAGTGTATCTCAAAATAGAAATTCCTGTTAGATATTC 2755
 DB TAAAGTGTGAGAGCCAGTGTATCTCAAAATAGAAATTTCTGTTAGATATTC 7688
 QY 2756 AGAATCTGTTATATGCTGTGATACATGTAAGAAACCCCATACCCGCAAAAGGCTC 2815
 DB AGAATCTGTTATATGCTGTGATACATGTAAGAAATCTATATCAGC-----AAAAGGCTC 7748
 QY 2816 TACCTTGAACATTAAGAGATTAACCAAGAGAGAAAGCCAAATTTATGTTCCAAATT 2875
 DB TACCTTTAA-----AATPAGCAATPACAAAGAGAGAAAGCCAAATTTATGTTCCAAAT 7801
 QY 2876 AGGCTTAACTTTTGAAGCAACTTTTGTAGCTGTGACATGAGAGAGCTGACT 2935
 DB TTAGGTTAACTTTTGAAGCAACTTTTGTAGCTGTGACATGAGAGAGCTGACT 7852
 QY 2936 CAGATTTGCTATGAGTTAATGAAGTCAAGCTGTGCTGAATPACATATGTTTCT 2995
 DB CAGATTTGCTATGAGTTAATGAAGTCAAGCTGTGCTGAATPACATATGTTTCT 7912
 QY 2996 CAGATTTGCTATGAGTTAATGAAGTCAAGCTGTGCTGAATPACATATGTTTCT 3055
 DB CAGATTTGCTATGAGTTAATGAAGTCAAGCTGTGCTGAATPACATATGTTTCT 7972
 QY 3056 AACTCATTAATACCTCTTCAAAATGCTTAATTCATTTCAACATTAATTTATCTGAG 3115
 DB AACTCATTAATACCTCTTCAAAATGCTTAATTCATTTCAACATTAATTTATCTGAG 8032
 QY 3116 TCTTGAAGCCAAATGAGTGTGATGGAATCAAGCTGTGCTGATCAGTCTGCT 3175
 DB TCTTGAAGCCAAATGAGTGTGATGGAATCAAGCTGTGCTGATCAGTCTGCT 8092
 QY 3176 TTTCTTTCTCTTTTACCAATTTTGTCTAAAGACAGTCTTCTCAACCTGCTGCTC 3235
 DB TTTCTTTCTCTTTTACCAATTTTGTCTAAAGACAGTCTTCTC-ATCACTTGTCTC 8152
 QY 3236 TCTATTTTGTATTTACTAGTTTAAAGATCAGAGTCACTTCTTGAAGTCTGCTATAT 3295
 DB TCTATTTTGTATTTACTAGTTTAAAGATCAGAGTCACTTCTTGAAGTCTGCTATAT 8211
 QY 3296 TTTCTTACCTGAACCTTTGCAAGTTTCAAGTAAACCTGAGTCAAGTCTGATTTAGC 3355
 DB TTTCTTACCTGAACCTTTGCAAGTTTCAAGTAAACCTGAGTCAAGTCTGATTTAGC 8271
 QY 3356 TCTCTTAAAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3386
 DB TCTCTTAAAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8331

RESULT 14
 US-09-949-293-25
 ; Sequence 25, Application US/09949293
 ; Publication No. US2003008250A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomann, Hans-Ulrich
 ; APPLICANT: Wall, Kristian
 ; APPLICANT: Fitzgerald, Michael
 ; TITLE OF INVENTION: MUTATIONS OF THE CYCLOOXYGENASE-2 GENE
 ; FILE REFERENCE: TECH01-07
 ; CURRENT APPLICATION NUMBER: US/09/949, 293

; CURRENT FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: 60/231,250
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 25
 ; LENGTH: 11064
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-949-293-25

Query Match 50.7%; Score 1717.4; DB 10; Length 11064;
 Best Local Similarity 95.8%; Pred. No. 0;
 Matches 1812; Conservative 0; Mismatches 61; Indels 18; Gaps 4;

QY	1497	TTACAGGAGAAAGAAATGTCTGAGAGATTTGAAAGCACTCTATGTGATCATCATGCTG	1556
DB	7899	TCACAGGAGAAAGAAATGTCTGAGAGATTTGAAAGCACTCTATGTGATCATCATGCTG	7958
QY	1557	TGAGACTGATCTGCTCCCTTCTGTAGAAAGCTCGGCGCATGCGCATCTTGGTGAA	1616
DB	7959	TGAGACTGATCTGCTCCCTTCTGTAGAAAGCTCGGCGCATGCGCATCTTGGTGAA	8018
QY	1617	CCATGCTAGAAATGAGACATCTCTCTTGAAGAGCTTATGCGTAAATGTTATATGTT	1676
DB	8019	CCATGCTAGAAATGAGACATCTCTCTTGAAGAGCTTATGCGTAAATGTTATATGTT	8078
QY	1677	CTCCTGCTACTGAGAGCCAGACACTTTTGTGAGAGAGTGGTTTTCAAAATCATCA	1736
DB	8079	CTCCTGCTACTGAGAGCCAGACACTTTTGTGAGAGAGTGGTTTTCAAAATCATCA	8138
QY	1737	CTGCTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGCTGTCCTTTACTTTCA	1796
DB	8139	CTGCTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGCTGTCCTTTACTTTCA	8198
QY	1797	GTTGTCAGATCCAGAGCTCATTTAAACATCAATCAATCAATGTTCTCCGCTCG	1856
DB	8199	GTTGTCAGATCCAGAGCTCATTTAAACATCAATCAATCAATGTTCTCCGCTCG	8258
QY	1857	GACTGATGATATCAATCCAGATCACTTAAGAAAGCGTGCAGCTGATGAACT	1916
DB	8259	GACTGATGATATCAATCCAGATCACTTAAGAAAGCGTGCAGCTGATGAACT	8318
QY	1917	CTAATGATCATATTAATTAATTAATGACAGCATCTATTAATTAATTAATTAAT	1976
DB	8319	CTAATGATCATATTAATTAATTAATGACAGCATCTATTAATTAATTAATTAAT	8378
QY	1977	ATTATATTAATCTCTTATGTTACTTAAATCTTCTGTTACAGAGTCACTCTCTGT	2036
DB	8379	ATTATATTAATCTCTTATGTTACTTAAATCTTCTGTTACAGAGTCACTCTCTGT	8438
QY	2037	TGCGGAGAAAGGAGTCATCTGTAAGAGCTTTATGTCACACTCTAAAGTTTTGCTG	2096
DB	8439	TGCGGAGAAAGGAGTCATCTGTAAGAGCTTTATGTCACACTCTAAAGTTTTGCTG	8498
QY	2097	TTGCTGTAGTTTGAAGAAAGCTTTTATCTGTTTAAACAGAGAAATGAGTT	2156
DB	8499	TTGCTGTAGTTTGAAGAAAGCTTTTATCTGTTTAAACAGAGAAATGAGTT	8558
QY	2157	TTGAGCTCTTTTACTGATTTCACTTAATTAATTAAGAGAAAGTAAAGTCTTTGA	2216
DB	8559	TTGAGCTCTTTTACTGATTTCACTTAATTAATTAAGAGAAAGTAAAGTCTTTGA	8618
QY	2217	ATACTTAACACTATCACAGATGCGAAATGCTGAAAGTTTTTACAGTGTGATGCTT	2276
DB	8619	ATACTTAACACTATCACAGATGCGAAATGCTGAAAGTTTTTACAGTGTGATGCTT	8678
QY	2277	CAATGATCTTCCATGATGATTAAGAGTAACTATGTTGAATTTTAAAGTCTTTG	2336
DB	8679	CAATGATCTTCCATGATGATTAAGAGTAACTATGTTGAATTTTAAAGTCTTTG	8738
QY	2337	GGTATTTTCTGTCTCAAC-AAAACAGTATCTGTCATTTAAATGAATTTAA	2395

DB	8739	GTTATTTTCTGTCAATCAAAAGAAAGAGTATCAGTGCATTTAAATGAATTTAA	8798
QY	2396	TTAGACATTTACAGTAATTTCAATGCTACTTTTAAATCAGCAATGAATTAATTTG	2455
DB	8799	TTAGACATTTACAGTAATTTCAATGCTACTTTTAAATCAGCAATGAATTAATTTG	8858
QY	2456	AAATTTCAATTCATGAGGATGAAATCACCTGTAAGAGCTGTTGATTTCTTAAGTTA	2515
DB	8859	AAATTTCAATTCATGAGGATGAAATCACCTGTAAGAGCTGTTGATTTCTTAAGTTA	8918
QY	2516	TTAAACTGTATACATATACCAAAAGAGCTGCTTGAATTAATCTGTAATTAATGATG	2575
DB	8919	TTAAACTGTATACATATACCAAAAGAGCTGCTTGAATTAATCTGTAATTAATGATG	8978
QY	2576	AAATTTACTACATATGCTTGTAAATATTTTAATGATGTTCTTTTACCAAGA	2635
DB	8979	AAATTTACTACATATGCTTGTAAATATTTTAATGATGTTCTTTTACCAAGA	9038
QY	2636	GTAATTAACCTTTTGTGATGCTTTAAACCTTCTTTAAATCAAAATGCAAAATTTAT	2695
DB	9039	GTAATTAACCTTTTGTGATGCTTTAAACCTTCTTTAAATCAAAATGCAAAATTTAT	9098
QY	2696	TAAAGTGTGAGCCATGCACTGATGTTATCTCAAAATTAATATCTGTTGATATTC	2755
DB	9099	TAAAGTGTGAGCCATGCACTGATGTTATCTCAAAATTAATATCTGTTGATATTC	9158
QY	2756	AGATCTGTTATATGCTGTGTAACATGTAATAAATCCCATACCCCGCAAAAGGCTCC	2815
DB	9159	AGATCTGTTATATGCTGTGTAACATGTAATAAATCCCATACCCCGCAAAAGGCTCC	9211
QY	2816	TACCTTAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATGTTCCAAATTT	2875
DB	9212	TACCTTAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATGTTCCAAATTT	9262
QY	2876	AGGTTTAACTTTTGAAGCAATTTTGTGACCTGTGACATGCAAGCTGTACT	2935
DB	9263	TTAGGTTTAACTTTTGAAGCAATTTTGTGACCTGTGACATGCAAGCTGTACT	9322
QY	2936	CAGATTTGCTATGAGTTAATGAATGACCAAGCTGTGCTGAATTAAGATATGTTTCT	2995
DB	9323	CAGATTTGCTATGAGTTAATGAATGACCAAGCTGTGCTGAATTAAGATATGTTTCT	9382
QY	2996	CAGATTTCTGTGACAGTTTAAATTTAGCAGTCCATATCAATGCAAAAGTACATG	3055
DB	9383	CAGATTTCTGTGACAGTTTAAATTTAGCAGTCCATATCAATGCAAAAGTACATG	9442
QY	3056	ACCTCATTAATTAACCTCTTCAAAATGCTTAATTAATTAATTAATTAATTAAT	3115
DB	9443	ACCTCATTAATTAACCTCTTCAAAATGCTTAATTAATTAATTAATTAATTAAT	9502
QY	3116	TCTTGAAGCAATTCAGTAAGTGCATGGAATCAAGCTGCTGATCTGATGCTGCTT	3175
DB	9503	TCTTGAAGCAATTCAGTAAGTGCATGGAATCAAGCTGCTGATCTGATGCTGCTT	9562
QY	3176	TTTCTTTCTTTTACCAATTTTGTGTAAGACACAGTCTTCAAAACCTTGCTTTC	3235
DB	9563	TTTCTTTCTTTTACCAATTTTGTGTAAGACACAGTCTTCAAAACCTTGCTTTC	9621
QY	3236	TCTATTTTGTGTTTACTGTTTAAAGATCAAGTTCATCTTCTTGAATCTGCTATAT	3295
DB	9622	TCTATTTTGTGTTTACTGTTTAAAGATCAAGTTCATCTTCTTGAATCTGCTATAT	9681
QY	3296	TTTCTTACCTGAACCTTGAAGTTTGAAGTAAACCTCAGTCAAGAGCTGATATATG	3355
DB	9682	TTTCTTACCTGAACCTTGAAGTTTGAAGTAAACCTCAGTCAAGAGCTGATATATG	9741
QY	3356	TCCTCTTAAGAAGATTAATAAAAAAAAAAAAAA 3386	
DB	9742	TCCTCTTAAGAAGATTAATAAAAAAAAAAAAAA 9772	

RESULT 15
 US-09-919-060-4

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 07:25:26 ; Search time 8126 Seconds

(without alignments)
12446.863 Million cell updates/sec

Title: US-08-064-271-11

Perfect score: 3387
Sequence: 1 GTCACGAGACCTCCACAGAG.....GATTAAAAAAAAAAAAAG 3387

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estdpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1437.2	42.4	2247	11 AK049923	Mus muscu
2	976.2	28.8	1201	13 BX363285	BX363285 BX363285
3	887.4	26.2	997	9 AL583668	AL583668 AL583668
4	814.8	24.1	968	13 BX370552	BX370552 BX370552

C	5	728	21.5	810	9	AI971172	AI971172 wr26a04.x
C	6	718.8	21.2	2132	14	CD014050	CD014050 90138391
C	7	713	21.1	2793	11	AK046457	AK046457 Mus muscu
C	8	703.4	20.8	744	14	CD365731	CD365731 UI-H-FT2-
C	9	685.4	20.2	808	14	CB960307	CB960307 AGENCOURT
C	10	674.2	19.9	701	9	AL710848	AL710848 DKFZp686N
C	11	672.2	19.8	707	14	CA309056	CA309056 UI-H-FT1-
C	12	663.2	19.6	1473	29	AY415140	AY415140 Homo sapi
C	13	662	19.5	662	9	AL710813	AL710813 DKFZp686J
C	14	657.2	19.4	1448	29	AY415141	AY415141 Pan trogl
C	15	642	19.0	1448	29	AY415142	AY415142 Mus muscu
C	16	629	18.6	663	10	BG055155	BG055155 na02005.
C	17	623	18.4	631	10	BE673090	BE673090 7d29b11.x
C	18	599	17.9	1766	14	CD014048	CD014048 90138112
C	19	571.4	16.9	573	12	BM129013	BM129013 i1f6d06.Y
C	20	571.2	16.9	605	9	AL691944	AL691944 DKFZp33C
C	21	570.8	16.9	581	12	BM128780	BM128780 i1f6d06.x
C	22	566.4	16.7	612	14	CA308732	CA308732 UI-H-FT1-
C	23	565.6	16.7	606	9	AL691954	AL691954 DKFZp313D
C	24	565	16.7	1040	10	BE785396	BE785396 601478114
C	25	563.8	16.6	567	14	CB146285	CB146285 K-EST0201
C	26	548.8	16.2	1770	14	CD014049	CD014049 90138252
C	27	545	16.1	565	13	BQ100978	BQ100978 i1j2d09.Y
C	28	544.2	16.1	602	9	AL712736	AL712736 DKFZp686K
C	29	540.6	16.0	559	13	BQ100700	BQ100700 i1j2d09.x
C	30	532.2	15.7	597	9	AL783660	AL783660 tu28a05.x
C	31	531.6	15.7	645	14	CF787487	CF787487 855389.MA
C	32	529	15.6	776	9	AV756509	AV756509 AV756509
C	33	507.2	15.0	949	12	BI689383	BI689383 603315826
C	34	506.4	15.0	1107	14	CK030311	CK030311 AGENCOURT
C	35	488.2	14.4	612	14	CB243167	CB243167 UI-CF-FN0
C	36	487.4	14.4	489	9	AL710680	AL710680 DKFZp686E
C	37	486.4	14.4	593	14	CF788077	CF788077 856797.MA
C	38	475.2	14.0	594	9	AI123006	AI123006 OK36c09.s
C	39	470.4	13.9	537	9	AI022012	AI022012 OW64D12.x
C	40	465	13.7	609	9	AA565385	AA565385 nk17d08.s
C	41	464	13.7	522	9	AA825346	AA825346 oe63d06.s
C	42	454.2	13.4	473	12	BM988211	BM988211 UI-H-CO0-
C	43	448.8	13.3	866	14	CA988090	CA988090 AGENCOURT
C	44	445.4	13.2	657	14	CF907989	CF907989 A0517D05-
C	45	444.4	13.1	617	9	AA649944	AA649944 ns55D05.s

ALIGNMENTS

RESULT 1
AK049923
LOCUS
DEFINITION
Mus musculus adult male hippocampus cDNA, RIKEN full-length
enriched library, clone:G630011G21
product:prostoglandin-endoperoxide synthase 2, full insert
sequence.
ACCESSION
AK049923
VERSION
AK049923.1 GI:26340647
KEYWORDS
HTC, CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PubMed
10349636
REFERENCE
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374

PUBMED REFERENCE AUTHORS	11042159 3 Shiata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komou,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsuno,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Matsuda,S., Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Chatsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN Integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	20530913 4 11076861 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
JOURNAL REFERENCE AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
JOURNAL REFERENCE AUTHORS	6 (bases 1 to 2247) Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanaoka,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Horii,F., Imocani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Komou,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,Y., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohseki,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akashira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission Physical (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopædia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/. Location/Qualifiers 1..2247
SOURCE	/organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM:DB:C630011G21" /db_xref="MGI:2417448" /db_xref="taxon:10090" /clone="C630011G21" /sex="male" /tissue_type="hippocampus" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 92..1906 /note="[unamed protein product; prostaglandin-endoperoxide synthase 2 (MGI:97798, GB NM_011198, evidence: BLASTN, 99% match=2243) putative" /codon_start=1
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Query Match	42.4%	Score 1437.2	DB 11	Length 2247
Best Local Similarity 80.6%		Pred. No. 8.8e-301		
Matches 1750	Conservative 0	Mismatches 393	Indels 27	Gaps 5
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QY	87	CCGCCGTGCAGATCTCGCCGCCGCCCTGCTGCTGTGTGCGCGTCTGAGCCATA	146	
Db	81	CCACCTCGCGATGCTCTTCGAGCTGTGCTGTCTGTGCGTGCCTGGGGCTGACGAG	140	
QY	147	CAGCAAAATCCCTGCTGTCCCAACCCATGTCAAAACCGAGGTGTATGTAGTGGAT	206	
Db	141	CAGCAAAATCCCTGCTGTCCATCAATCAATGTCAAAACCGTGGGAAATGATAGCA	200	
QY	207	TTGACAGATTAATGCGATTTGTACCCCGACAGAGATTTATGAGAAAACCTGTCAAC	266	
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QY	267	CGGAATTTTGTACAGAATAAATATTTCGAAACCCACTCCAAACAGTGCATYAC	326	
Db	261	CTGAATTTGTACAGAATCAAAATTTACTGTGAAAGCCACCCCAACACAGTGACATYAC	320	
QY	327	TACTTACCCACTTCAAGAGATTTTGGAAAGCTGTGATTAATCATTCCTTCCTTGAATG	386	
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QY	387	CAATTATGATTTATGTGTGATCCAGATCCATTTGATTTGACAGTCCACCACTTAC	446	
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QY	447	ATGTGACTATGCTCAAAAAGCTGGGAACCTTCTTAACCTCTCTATTATCTTAGAG	506	
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QY	507	CCCTTCTCTGTGCTGTGATTTGCCCGACTCCCTTGAGGTGTCAAAAGGTAAAAAGCAG	566	
Db	501	CCCTTCTCTGTGAGATGATGCTGCCCACTCCCAATGGGTGTGAAAGGAAATAGAGAGC	560	
QY	567	TTCTGATTTCAATGATTTGTGAAAAAATTCCTTCTTAAGAAAGAAAGTTATCCTGATC	626	
Db	561	TTCTGATTTCAAAAAGATGCTGAAAAAGGATTTCTTAAGAAAGAAAGTTATCCTGATC	620	
QY	627	CCGAGGCTCAAAACATGATTTTGTCAATCTTTGCCAGCACTTCAAGCAACGATTTTCA	686	
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QY	687	AGACAGATCTAAGCGAGGCGCAGCTTTTCAACCAAGGCTGGGCCATGGAGTGAATTAA	746	
Db	681	AGACAGATCTAAGCGAGGCGCAGCTGGGTTCACCCAGAGGCTGGGCCATGGAGTGAATTAA	740	
QY	747	ATCATTTTACGGTGAACCTGGCTAGACAGGTAAACCTGGGCTTTTCAAGATGGAA	806	
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Db	801	AAATGAATATCAGGTCAATTTGGTGAAGATGATCCCCCAAGTCAAGAATACTCAG	860	
QY	867	CAGAGTATCTACCTCTCAAGTCCCTGAGCATTAAGGTTTGTGTGGGGCAGGAG	926	

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 Db 134 AAGCTACCCCGCGCGCGCCGCTGCGCGCTGCGATGTCGCCCGCGCGCTGCT 193
 QY 121 GTGCGCGCTCTGCGCTGCGCGCTGCGATGTCGCCCGCGCGCTGCT 180
 Db 194 GTGCGCGCTCTGCGCGCTGCGCGCTGCGATGTCGCCCGCGCGCTGCT 253
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 Db 434 GAATTAATTCCTCTCTGCGAAATGCAATTAATGATGATGATGATGATGAT 493
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 QY 901 TCTAAGGTTCCTGCGGCGAGAGCTTTGATGATGATGATGATGATGATGAT 960
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RESULT 3
 AL583668
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 691.r. For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DK012CD04QPLcluster=691.r. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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 Location/Qualifiers
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 /note="1st strand cDNA was primed with a NotI-oligo (dt)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 26.2%; Score 887.4; DB 9; Length 997;
 Best Local Similarity 91.3%; Pred. No. 1.4e-181;
 Matches 852; Conservative 70; Mismatches 11; Indels 0; Gaps 0;
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 Db 65 GTCCAGGAATCTCTCAGAGAGGCTCTCTTCAAGCTCAGACGACGCTTCA 124
 QY 61 AAGCTACCCCGCGCGCGCCGCTGCGCGCTGCGATGTCGCCCGCGCGCTGCT 120
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Db	425	GAATMACATTCCTTTCCTTGAAATKCAATTATAGTATTATGTGGATGTGGACATTCAGATTACA	484
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Db	485	TTTGATTGACAGTACACCACTTCCAAAGCTGACTGATCTGCTTCAAAAGCTGGAAAGCCTT	544
QY	481	CTCTAACTCTTCCTATTATATCTAGAGCCCTTCCTCGTGTGCTGATATGTTGCGCGACTCC	540
Db	545	CTCTAACTCTTCCTATTATATCTAGAGCCCTTCCTCGTGTGCTGATATGTTGCGCGACTCC	604
QY	541	CTTGCGGTCTCAAAAGTTAAAGACAGCTTCTGATTCCAATGATGTTGTGAAAAATGCT	600
Db	605	CTTGCGGTCTCAAAAGTTAAAGACAGCTTCTGATTCCAATGATGTTGTGAAAAATGCT	664
QY	601	CTTAAGAAAGAAAGTTTCATCCCTGATTCGCCAGGCGTCAAAACATGATGTTTGCATCTTTC	660
Db	665	TTTAAAGAAAGAAAGTTTCATCCCTGATTCGCCAGGCGTCAAAACATGATGTTTTC	724
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QY	721	CGGCTGCGGCATGCGGCTGTGACTTAATATCATATTTACGCTGAAAACTGTGCTAGACAGCG	780
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QY	901	TCTACGGTTTCTGTGGGGGCGAGAGCTTTGG	933
Db	965	TCTWCGGTTTCTGTGGGGGCGAGAGGKCTTTKG	997
RESULT 4			
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DEFINITION	BX370552 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens		
ACCESSION	BX370552		
VERSION	BX370552.1	GI:30457926	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	Unpublished (2001)		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	BP 191 91006 Evry cedex - France		
	Email: seqref@genoscope.cns.fr, Web : ww.genoscope.cns.fr		
	Library was constructed by life technologies, a division of		
	Invitrogen. This sequence belongs to sequence cluster 691.r For		
	more information about this cluster, see		
	http://www.genoscope.cns.fr/		
	cgi-bin/cluster.cgi?seq=CS0BA0492A07_CS04657_1&cluster=691.r.		
	Contact : Feng liang Email : fliang@lifetech.com URL :		
	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600		
	Faraday Avenue Genoscope sequence ID : CS0BA0492A07_CS04657_1.		
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Query Match	24.1%	Score 814.8	DB 13	Length 968
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Matches	896	Conservative	0	Mismatches 62; Indels 4; Gaps 4;
ORIGIN				
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QY	825	TTGATGAGAGATGTATCTCTCCACAGTCACAAAGATATCTACGAGAGATGATCTACCTC	884	
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QY	885	CTCAAGTCCCTGAGACATCTACGATTTGCTGCGGGGAGAGAGTCTTTGTTGCTGCTG	944	
DB	66	CTCAAGTCCCTGAGACATCTACGATTTGCTGCGGGGAGAGAGTCTTTGTTGCTGCTG	125	
QY	945	GTCGTGATGATGTATCCCAATCTGCGCTGCGGGAACAACAAGATGTGATGTGCTTA	1004	
DB	126	GTCGTGATGATGTATCCCAATCTGCGCTGCGGGAACAACAAGATGTGATGTGCTTA	185	
QY	1005	AACAGGAGACATCTCGAATGGGGGTATGATGAGAGCTTTGTTCCAGACAAGAGGTATATCTGA	1064	
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QY	1065	TAGAGAGACTATTAAAGATTGTGATGAAGATTATGTGCAACACTGATGATGCTATCACT	1124	
DB	246	TAGAGAGACTATTAAAGATTGTGATGAAGATTATGTGCAACACTGATGATGCTATCACT	305	
QY	1125	TCAACCTGAATTTGACCCGGAATCTCTTTCAACAACAATTCACAGTACCAAAATGCTA	1184	
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QY	1185	TTGCTGCTGAATTTAAACACCTCTCATCATCTGGACATCCCTTCTCCTGACACCTTTGAA	1244	
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QY	1245	TTCATGACCAAAATCAACTATCAACAAGTTATCTACAAACTCTATATTTGCTGAAAC	1304	
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DB	486	ATGGAATTTACCAAGTTTGTGAATCATTCACACGACAAATTTGCTGAGAGGTTCTGCTG	545	
QY	1365	GTAGGAATGTTCCACCCGCACTACAGAAAGTATCAACAGCTTCCATTGACCAAGACGAC	1424	
DB	546	GTAGGAATGTTCCACCCGCACTACAGAAAGTATCAACAGCTTCCATTGACCAAGACGAC	605	
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DB	606	AGATGAATATCCAGCTTTTAAATAGATACCGCAAAAGCTTATATGCTGAAGCCCTATGAAT	665	
QY	1485	CA-TTTGAAGAATCTTACAGAGAAAGAAATGTCTGACAGTTTGAAGACCTATATGAT	1543	
DB	666	TATTTTGAAGAACTTACAGAGAGAAAGAAATGTCTGACAGTTTGAAGACCTATATGAT	725	
QY	1544	GACATCCATGCTGTGAGAGCTGATATCTGAGCTTCTGTGAGAAAGAGCTCGGACAGATGCC	1603	
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QY	1604	ATC-TTTGGTAAAAACATGATAGAAAGTTGAGACACATTTCTCTTGAAGAAGACTTATGGG	1662	
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QY	1663	TAA-TGTTATATG-TTCTCTGCTCTACTGGAAGCCAAAGCACTTTTGTGTGAGAAAGTGGT	1720	
DB	846	GAAAGGTATATGTTTCTCTGCTCTACTGGAAGCCAAAGCACTTTTGTGTGAGAAAGTGGT	905	

QY 1721 TTGCAATCATCAACAGTCCTGATTCAGTCTCTCATCTGCAATTAACGTGAAGGCTGT 1780
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 QY 1781 CC 1782
 Db 966 CC 967

RESULT 5
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 A1971172
 VERSION A1971172.1 GI:5767998
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 COMMENT Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-1@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at: www.bio.illn.gov/bbrp/image/image.html
 Insert length: 1260 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 450.
 Location/Qualifiers
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 /clone="IMAGE:2488782"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Pz28"
 /note="Organ: prostate; Vector: pTZ19-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP_Pz22 was prepared, and ss circles were used in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 21.5%; Score 728; DB 9; Length 810;
 Best Local Similarity 95.5%; Pred. No. 5.1e-147;
 Matches 760; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 1741 CTCGAATTCAGTCTCTGCAATTCGCAATTAACGGAGGCTGCTTCTTACTTCACTGCTGT 1800
 Db 796 CTCGATTCAGTCTCTCTCATCTGCAATTAACGGAGGCGGCCCTGTACTTCACTGCTGT 737

QY 1801 TCCGATCCGAGAGCTCTTAAACAGTCACTTAATGCAAGTTCTTCCGCTCCGAGCT 1860
 Db 736 TCCGATACGAGAGCTCTTAAAGCAAGTCACTTAATGCAAGTTCTTCCGCTCCGAGCT 677

QY 1861 AGATGATATCAATCCACAGTACTACTTAAAGAAAGCGTGCATGAACTGTGAAGCTTAA 1920
 Db 676 AGATGATATCAATCCACAGTACTACTTAAAGAAAGCGTGCATGAGTGTGAAGCTTAA 617
 QY 1921 TGATCATATTAATTAATTAATGAGAACAGTGTCTTAAATTAATTAATTAATTAATTT 1980
 Db 616 TGATCATATTAATTAATTAATGAGAACAGTGTCTTAAATTAATTAATTAATTAATTT 557
 QY 1981 ATATTTAACTCTTATGTTACTTAACATCTCTGTAAACAGAGTCACTGCTGTCG 2040
 Db 556 ATATTTAACTCTTATGTTACTTAACATCTCTGTAAACAGAGTCACTGCTGTCG 497
 QY 2041 GAGAAAGAGTCACTGTTGTAAGACTTTTATGTCATCTCTTAAAGTTTGTGTCG 2100
 Db 496 GAGAAAGAGTCACTGTTGTAAGACTTTTATGTCATCTCTTAAAGTTTGTGTCG 437
 QY 2101 TGTTAAGTTTGAAGAAAGTTTATCTGTTTATTAAGCAGAGAGAAATGAGTTTGA 2160
 Db 436 TGTTAAGTTTGAAGAAAGTTTATCTGTTTATTAAGCAGAGAGAAATGAGTTTGA 377
 QY 2161 CGTCTTTTACTGTAATTTCACTTAATTAATTAAGAGAAAGTAAAGTGTGGAATAC 2220
 Db 376 CGTCTTTTACTGTAATTTCACTTAATTAATTAAGAGAAAGTAAAGTGTGGAATAC 317
 QY 2221 TTAAGACTATCAAGAAAGTGCAGAAATGCTGAAGTTTACACTGTCGATGTTCCAT 2280
 Db 316 TTAAGACTATCAAGAAAGTGCAGAAATGCTGAAGTTTACACTGTCGATGTTCCAT 257
 QY 2281 GCATCTTCATCAAGTATGATTAAGTAACTAATGTTTGAATTTTAAAGTACTTTGGGTA 2340
 Db 256 GCATCTTCATCAAGTATGATTAAGTAACTAATGTTTGAATTTTAAAGTACTTTGGGTA 197
 QY 2341 TTTTCTGTGATCAAC-AAACAGTATGATGATTAATTAATTAATTAATTAATTAAG 2399
 Db 196 TTTTCTGTGATCAACAAACAAACAGTATGATGATTAATTAATTAATTAATTAATTAAG 137
 QY 2400 ACATTAACAGTAATTTATGATGATTAATTAATTAATTAATTAATTAATTAATTAAT 2459
 Db 136 ACATTAACAGTAATTTATGATGATTAATTAATTAATTAATTAATTAATTAATTAAT 77
 QY 2460 TTCTAATTCATAGGGTAGATCACTGTAAGAGCTGTGATTTCTTAAGTTATTA 2519
 Db 76 TTCTAATTCATAGGGTAGATCACTGTAAGAGCTGTGATTTCTTAAGTTATTA 17
 QY 2520 ACTTGTACATATACCA 2535
 Db 16 AATAGTACATATACCA 1

RESULT 6
 LOCUS CD014050 2132 bp mRNA linear EST 21-OCT-2003
 DEFINITION 90138391 Single gene library Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD014050
 VERSION CD014050.1 GI:37777580
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE 1 (bases 1 to 2132)
 AUTHORS Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R., Au-Yang, J., and Stuve, L.L.
 JOURNAL PCR isolation and cloning of novel splice variant mRNAs from known drug target genes
 COMMENT Unpublished (2003)
 CONTACT: Jin, P.
 INCYTE Corporation
 3160 Porter Drive, Palo Alto, CA 94304, USA
 Tel: 650 621 8639
 Fax: 650 621 8965
 Email: pjine@incyte.com.

FEATURES
Source

Location/Qualifiers
1. 2132
/organism="Homo sapiens"
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/db xref="taxon:9606"
/clone_lib="Single gene library"
/note="Vector: pDrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencing using primers flanking the gapped areas."

ORIGIN

Query Match 21.2%; Score 718.8; DB 14; Length 2132;
Best Local Similarity 65.0%; Pred. No. 4.4e-145;
Matches 1078; Conservative 0; Mismatches 577; Indels 3; Gaps 1;

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212 CAGTATAGT 271
425 CGCTACAGT 484
272 TTTTGAAGAATAAATTTATTTCTGTGAACCACTCCAAACAGAGTCACTACTT 331
485 CTGTGACCTGT 544
332 ACCCACTTCAAGGAGTTTGTGAAGTGTGTGAATTAATTCCTCTTCCGAAATGCAATT 391
545 ACTCACGCGGCTGT 601
392 ATGATGATGT 451
602 ATGCGCTGT 661
452 GACTATGCTTCAAAAAGTGTGAAGCTTCTTAACCTCTCTTAATTAATAGAGCCCTT 511
662 GCAATATGATGT 721
512 CTTCTGT 571
722 CCTCTGT 781
572 GATCAATGATGT 631
782 GATGCCAGCTCTGT 841
632 GGCTCAAAACATGATGT 691
842 GGACCAACCTGATGT 901
692 GATCAATGAGGAGGCGCACTTTTCAACAACGAGGCTGTGTGTGTGTGTGTGTGTGTGTGT 751
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752 ATTATGAGTGAATCTGT 811
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812 AAATATGATGAATTTGT 871
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932 GGT 991
1142 GGGGT 1201

992 TGTGATGTGCTTAAACAGAGCATCTGTAATGGGGTGTATGAGCAGTTGTTCCAGCAAGC 1051
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1052 AGGCTAATGATGATGAGAGACTTATTAAGATTGTGTATGATTAATGATTAATGATTAATG 1111
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1652 GACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1711
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1712 GAAGT 1771
1922 GAGGT 1981
1772 AAGGCTGT 1831
1982 AAGGCTGT 2019

RESULT 7
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DEFINITION
AK046457 2793 bp mRNA linear HTC 20-SEP-2003
Mus musculus adult male corpora quadrigemina cDNA, RIKEN
full-length enriched library, clone: B230387B01
product: prostaglandin-endoperoxide synthase 1, full insert
sequence.
ACCESSION
AK046457
VERSION
AK046457.1 GI: 26338102
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1

AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 9279253
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 2049374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, U., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, T.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 MEDLINE 11700000
 PUBMED 11700000
 REFERENCE 5
 AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 MEDLINE 12000000
 PUBMED 12000000
 REFERENCE 6 (bases 1 to 2793)
 AUTHORS Aachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp,
 url: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 location/Qualifiers
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 Best Local Similarity 64.2%; Pred. No. 7.7e-14;
 Matches 1089; Conservative 0; Mismatches 605; Indels 3; Gaps 1;
 111 CCCTGCTGCTGTGGCGCGTCTGCGCTGACCAATGAGCAATCTGTGTTCCACC 170
 129 CTTGCGTCTGCTGCGAGATCTGGGTTGCCCTGACGATCAATCCCTGTTTACATC 188
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 651 CATCTTTGGCCAGCACTTCAAGCAAGTTTTCAGAGATCATTAAGGAGGCGCAG 710

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Db	726	GCTTTACCAAGGCTCTTAGGCCACGGGGGTAGACCTTGGCCACATTTATGGAGATACTGG	785
Qy	771	CTAGACAGCGTAACTCGGCTCTTTTCAAGATGGAATAAATGAATAATACGATATTTGATG	830
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Qy	831	GAGAGATGTATCCCTCCACAGTCAAAATACTACAGGACAGATGATCTACCTCTCAAG	890
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Qy	891	TCCCTGAGCATCTACGGTTTCTGTGGGGACGAGAGTCTTTTGGTCTGGTGCCGTGTGA	950
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Qy	951	TGATGTATGCGCAATCTGGCTGGGGGAAACAAACAGATGTGTGATGTGTCCTTAACAGG	1010
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Qy	1491	AAGAACTTACAGAGAAAAAGAAATGTCTGCAAGTTTGAAGCACTCTATGTGACATGC	1550
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[illegible]

RESULT 10
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DEFINITION AL710848 701 bp mRNA linear EST 04-SEP-2003
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AL710848
ACCESSION
VERSION AL710848.1 GI:19694203
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
REFERENCE
AUTHORS
TITLE EST (Duesterhoeft, et al.)
JOURNAL
COMMENT Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKEZp686N0473) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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ORIGIN
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Best Local Similarity 99.3%; Pred No. 2.4e-135;
Matches 698; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
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871 GATGATCTACCTCCCTCAAGTCCCTGAGATCTACAGGTTGCTGGGGGAGAGAGTCTT 930
240 GATGATCTACCTCCCTCAAGTCCCTGAGATCTACAGGTTGCTGGGGGAGAGAGTCTT 299
931 TGGTCTGGTGGCTGGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 990
300 TGGTCTGGTGGCTGGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
991 ATGTGATGCTGTTAAACAGAGCATCTGTAATGAGGATGAGAGGTTGTTCCAGACAG 1050

Db 360 ATGGCATGTGCTTAAACAGAGCATCTGTAATGAGGATGAGAGGTTGTTCCAGACAG 419
Qy 1051 CAGGCTAATAGTATAGAGAGACTATTAAGTTGATTTGAAGTTATGTCACACTT 1110
Db 420 CAGGCTAATAGTATAGAGAGACTATTAAGTTGATTTGAAGTTATGTCACACTT 479
Qy 1111 GAGTGGCTATCAGTTCAACAGAAATTTGACCCAGAACTACTTTTCAACAAACAAATTCGA 1170
Db 480 GAGTGGCTATCAGTTCAACAGAAATTTGACCCAGAACTACTTTTCAACAAACAAATTCGA 539
Qy 1171 GTACCAAAATGATGATGCTGCTGATTTAAACACCTCTATCATCTGGGATCCCTCTGCC 1230
Db 540 GTACCAAAATGATGATGCTGCTGATTTAAACACCTCTATCATCTGGGATCCCTCTGCC 599
Qy 1231 TGACACCTTTCAAAATTCATGACCAAGATTAACACTATGACAGGTTATCTACAAACACTC 1290
Db 600 TGACACCTTTCAAAATTCATGACCAAGATTAACACTATGACAGGTTATCTACAAACACTC 659
Qy 1291 TATATTGCTGGAACATGGAATTAACCACTTTGTTGAATCATTC 1333
Db 660 TATATTGCTGGAACATGGAATTAACCACTTTGTTGAATCATTC 701

RESULT 11
CA309056/c
LOCUS
DEFINITION CA309056 707 bp mRNA linear EST 01-NOV-2002
UI-H-F11-Bie-1-15-0-UI.s1 NCI CGAP F11 Homo sapiens cDNA clone
UI-H-F11-Bie-1-15-0-UI 3', mRNA sequence.
CA309056
VERSION CA309056.1 GI:24472110
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE NCI-CGAP
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 550-627, >(TAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
1..707
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-F11-Bie-1-15-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP F11"
/note="Organ: Lung; Vector: pT7H1B-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP F11 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7H1B-Pac vector. The oligonucleotide used to prime the

synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)₁₈ tail. The sequence tag for this library is GGGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG TISSUE=Human Lung Ateolar Macrophage TAG LIB=UI-H-PT1 TAG_SEQ=GGGCATGCCG"

Query Match 19.8%; Score 672.2; DB 14; Length 707;
Best Local Similarity 98.7%; Pred. No. 6,4e-135;
Matches 688; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

1847 TCCCGCTCCGCGATAGATGATATCCACAGTACTACTATAAAGAGCGTGCAGTAA 1906
Db TCCCGCTCCGCGATAGATGATATCCACAGTACTACTATAAAGAGCGTGCAGTAA 1906
1907 CTGTAGAGCTAATGATCATATTTATTTATTTATTTATTTATTTATTTATTTATTT 1966
Db CTGTAGAGCTAATGATCATATTTATTTATTTATTTATTTATTTATTTATTTATTT 1966
1967 ATTATATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2026
Db ATTATATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2026
587 ATTATATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 528
Db ATTATATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 528
2027 GTACTCTGTGGGAGGAGAGAGTATCTGTGAGAGCTTTATGCTACTACTATA 2086
Db GTACTCTGTGGGAGGAGAGAGTATCTGTGAGAGCTTTATGCTACTACTATA 2086
527 GTACTCTGTGGGAGGAGAGAGTATCTGTGAGAGCTTTATGCTACTACTATA 468
Db GTACTCTGTGGGAGGAGAGAGTATCTGTGAGAGCTTTATGCTACTACTATA 468
2087 GATTTTGTCTGTGCTGTATGATTTGAAAAAGTTTATTCGTTTATTAACAGAGA 2146
Db GATTTTGTCTGTGCTGTATGATTTGAAAAAGTTTATTCGTTTATTAACAGAGA 2146
467 GATTTTGTCTGTGCTGTATGATTTGAAAAAGTTTATTCGTTTATTAACAGAGA 408
Db GATTTTGTCTGTGCTGTATGATTTGAAAAAGTTTATTCGTTTATTAACAGAGA 408
2147 GAAATGAGTTTGTGAGCTTTTATCTGTAATTTCACTTATTTATTAAGAGAGATA 2206
Db GAAATGAGTTTGTGAGCTTTTATCTGTAATTTCACTTATTTATTAAGAGAGATA 2206
407 GAAATGAGTTTGTGAGCTTTTATCTGTAATTTCACTTATTTATTAAGAGAGATA 348
Db GAAATGAGTTTGTGAGCTTTTATCTGTAATTTCACTTATTTATTAAGAGAGATA 348
2207 AGATGTTTGAATCTTAAACATATCAAGATGCGAAATGCTGAAAGTTTTCACATG 2266
Db AGATGTTTGAATCTTAAACATATCAAGATGCGAAATGCTGAAAGTTTTCACATG 2266
347 AGATGTTTGAATCTTAAACATATCAAGATGCGAAATGCTGAAAGTTTTCACATG 288
Db AGATGTTTGAATCTTAAACATATCAAGATGCGAAATGCTGAAAGTTTTCACATG 288
2267 TCGATGTTTCAATGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 2326
Db TCGATGTTTCAATGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 2326
287 TCGATGTTTCAATGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 228
Db TCGATGTTTCAATGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 228
2327 AGTACTTTGGGTATTTTCTGTCATCAAC-AAAAAGGTATCGTGCATTTTAAATG 2385
Db AGTACTTTGGGTATTTTCTGTCATCAACAAAAAGGTATCGTGCATTTTAAATG 2385
227 AGTACTTTGGGTATTTTCTGTCATCAACAAAAAGGTATCGTGCATTTTAAATG 168
Db AGTACTTTGGGTATTTTCTGTCATCAACAAAAAGGTATCGTGCATTTTAAATG 168
2386 AATATTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2445
Db AATATTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2445
167 AATATTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 108
Db AATATTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 108
2446 CAATATTTGAAATTTCTPAATTCATAGGGTGAATCACTGTAAAGCTGTGTGATTT 2505
Db CAATATTTGAAATTTCTPAATTCATAGGGTGAATCACTGTAAAGCTGTGTGATTT 2505
107 CAATATTTGAAATTTCTPAATTCATAGGGTGAATCACTGTAAAGCTGTGTGATTT 48
Db CAATATTTGAAATTTCTPAATTCATAGGGTGAATCACTGTAAAGCTGTGTGATTT 48
2506 CTAAAGTTATTAACCTGTACATATACCAAAAAA 2542
Db CTAAAGTTATTAACCTGTACATATTCACAAAAA 11

RESULT 12
AY415140 1473 bp DNA linear GSS 17-DEC-2003
LOCUS AY415140
DEFINITION Homo sapiens PTGS1 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY415140
VERSION AY415140.1 GI:39771099
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
gene
ORIGIN

Query Match 19.6%; Score 663.2; DB 29; Length 1473;
Best Local Similarity 66.7%; Pred. No. 5.2e-133;
Matches 947; Conservative 0; Mismatches 473; Indels 0; Gaps 0;

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Db CAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 124
65 CAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 124
Db TTCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 569
125 TGCCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 184
Db CTGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 629
570 CTGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 629
185 CAGATGCGGACTCTGCGCGCGCGCGCTTCTGCTGAGAGAGATGATGATGATGATGATG 244
Db AGGCTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 689
630 AGGCTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 689
Db AAGGACCAACCTCATGTTGCTTCTTGCACAAACATTCACCAACACAGTTCTTCAAA 304
245 AAGGACCAACCTCATGTTGCTTCTTGCACAAACATTCACCAACACAGTTCTTCAAA 304
Db CAGATCAACAGAGGCGGCTTTCACCAAGGCTTTCACCAAGGCTTTCACCAAGGCTTTC 749
690 CAGATCAACAGAGGCGGCTTTCACCAAGGCTTTCACCAAGGCTTTCACCAAGGCTTTC 749
Db CTTTCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 364
305 CTTTCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 364
Db ATATTTACGTTGAATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 809
750 ATATTTACGTTGAATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 809
Db ACATTTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 424
365 ACATTTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 424
Db TGAATATCAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 869
810 TGAATATCAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 869
Db TCAAGTACCAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 484
425 TCAAGTACCAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 484
Db AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 929
870 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 929
Db TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 544
485 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 544
Db TTGCTGCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 989
930 TTGCTGCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 989

Db 545 TTGGGCTGCTTCTGGGCTCATGCTGTATGCAAGCTTGGCTAGTGAACAACCCGTG 604
 QY 990 TATGTGATGTCTTAAACAGAGCATCTGAATGGGGTATGAGCAGTGTGTCAGACAA 1049
 Db 605 TGTGTGACCTGCTGAAGCTGACACCCACTGGGGGATGAGAGCTTTTCCAGACGA 664
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 Db 665 CCCGCTCATCTCATAGGGAGACCAATCAAGATTGATCATGAGAGATCACTGACAGC 724
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 Db 725 TGAAGTGTATTTCTCGAGTGAATTTGACCAAGCTGCTTTGGTGTCCAGTTCC 784
 QY 1170 AGTTCGAAATTCGATTTGCTGCTGAATTTAACACCTCTATACCTGTCATCCCTTTCG 1229
 Db 785 AATACCCCAACCGCATTCAGATGAGATTTCAACATCTCTACCTGAGCACTCCCTCATGC 844
 QY 1230 CTGACACCTTCAATTCATGACCAAGAAATTCACATTCACAGTTTATCTACACACT 1289
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 QY 1290 CTATATGCTGGAACATGAAATTAACAGTTTGTGATCATTCACACAGGCAATGCTG 1349
 Db 905 CCAATGTTGATGATGATGGGGTGAAGCCCTGATGATGCTTCTTCGCGCAATTTGCT 964
 QY 1350 GCAGGCTGCTGCTGTGATGAGAAATGTTCCACCCGAGTACAGAAATATCAAGGCTTCCA 1409
 Db 965 GCGGATCGGTGGGGGAGGAAACATGACCAACCATCTGACATGTCGCTGGAATGTCA 1024
 QY 1410 TTGACCAAGACAGGAGATGAATACCATGCTTTTATGATGATCCGAAACGCTTTATGC 1469
 Db 1025 TCGAGGAGTCTCGAGAGATCGGCTGACGCTTCATGATGATGATGATGATGATGATG 1084
 QY 1470 TGAAGCTTATGATATCTTGAAGAACTTACAGAGAGAGAGAGAGAGAGAGAGAGAG 1529
 Db 1085 TGAACCTTACACTCTCTTCCAGAGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1144
 QY 1530 AAGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1589
 Db 1145 AGGAATGTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1204
 QY 1590 CTGGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1649
 Db 1205 GGCATCCAACTTATCTTGTGGAGAGATGATGATGATGATGATGATGATGATGATGATG 1264
 QY 1650 AAGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1709
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 QY 1770 TGAAGGCTGCTGCTTACTTCAATTCAGTGTTCACATTC 1809
 Db 1385 CCAAGACTGTCTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1424

RESULT 13
 AL710813 662 bp mRNA linear EST 04-SBP-2003
 LOCUS AL710813
 DEFINITION DKF2p686J1373.1 686 (synonym: h1cc3) Homo sapiens cDNA clone
 DKF2p686J1373.5', mRNA sequence.
 ACCESSION AL710813
 VERSION AL710813
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 662)
 AUTHORS Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and

TITLE JOURNAL COMMENT

Wiemann, S.
 Est (Duesterhoeft, et al.)
 Unpublished (1999)
 Contact: MIPS

MIPS
 Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
 consortium of the German Genome Project.
 No sequence available.
 This clone (DKF2p686J1373) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clonezpd.de.

FEATURES

source

1. 662
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKF2p686J1373"
 /dev_stage="adult"
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 /note="vector: pTriplex2; Site_1: SfiI; Site_2: SfiIb;
 cDNA-collection"

ORIGIN

Query Match 19.5%; Score 662; DB 9; Length 662;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
 Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 GGGTATGAGCACTTGTTCAGACAGCAGGCTTAATCTGATGAGAGACTTAAAT 60
 QY 1084 TGTGATGAGATTTATGTCACACTTGTGCTATCACTTCAACTGAATTTGACCC 1143
 Db 61 TGTGATGAGATTTATGTCACACTTGTGCTATCACTTCAACTGAATTTGACCC 120
 QY 1144 AGAATCTATTTTCAACAAATTCAGATCCAAATCGTATGCTGCTGAATTTAAC 1203
 Db 121 AGAATCTATTTTCAACAAATTCAGATCCAAATCGTATGCTGCTGAATTTAAC 180
 QY 1204 CCTCTATCACTGGCAATCCCTCTGCTGACACCTTCAATTCATGACCAAGAAATCA 1263
 Db 181 CCTCTATCACTGGCAATCCCTCTGCTGACACCTTCAATTCATGACCAAGAAATCA 240
 QY 1264 CTATCAACAGTTTATCTACAACTCTATTTGCTGGAACATGAAATTAACCACTTTG 1323
 Db 241 CTATCAACAGTTTATCTACAACTCTATTTGCTGGAACATGAAATTAACCACTTTG 300
 QY 1324 TGAATATTTACACAGCAATTTGCTGAGGGTGTGCTGATGAGAAATGTTCCACCCG 1383
 Db 301 TGAATATTTACACAGCAATTTGCTGAGGGTGTGCTGATGAGAAATGTTCCACCCG 360
 QY 1384 AGTACAGAAAGTATCACAGGCTTCAATGACAGAGCAGAGCAATTAACCACTTT 1443
 Db 361 AGTACAGAAAGTATCACAGGCTTCAATGACAGAGCAGAGCAATTAACCACTTT 420
 QY 1444 TATAGTATCCGCAACGCTTTATGCTGAGCCCTATGATGATTTGAAGAACTTACAG 1503
 Db 421 TATAGTATCCGCAACGCTTTATGCTGAGCCCTATGATGATTTGAAGAACTTACAG 480
 QY 1504 AGAAAAAGAAATGCTGCGAGATTTGAGAGCACTTATGCTGACATGATGCTGTGAGGT 1563
 Db 481 AGAAAAAGAAATGCTGCGAGATTTGAGAGCACTTATGCTGACATGATGCTGTGAGGT 540
 QY 1564 GTATCTGCGCTTGTGTAAGAGCTGCGAGATGCAATGCTTTGGTGAAGCAATGAT 1623
 Db 541 GTATCTGCGCTTGTGTAAGAGCTGCGAGATGCAATGCTTTGGTGAAGCAATGAT 600
 QY 1624 AGAAGTTGAGAGCACTTCTCTTGAAGAACTTATGATGATGATGATGATGATGATGATG 1683

D6		601	AGAGTTGGACGACCATTCTCTTGAAAGACTTATGGTAATGTATATGTTCTTCGC	660
OY	1684	CT	1685	
D6	661	CT	662	
<hr/>				
RESULT 14				
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LOCUS	Pan troglodytes PTGS1 gene, VIRUAL TRANSCRIPT, partial sequence,			
DEFINITION	Genomic survey sequence.			
VERSION	AY415141			
KEYWORDS	AY415141.1 GI:39771100			
SOURCE	GSS.			
ORGANISM	Pan troglodytes (chimpanzee)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.			
TITLE	(1 bases 1 to 1448)			
JOURNAL	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,			
PUBMED	Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,			
REFERENCE	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,			
AUTHORS	Adams,M.D. and Cargill,M.			
TITLE	Interfering nonneutral evolution from human-chimp-mouse orthologous			
JOURNAL	gene tries			
PUBMED	Science 302 (5652), 1960-1963 (2003)			
REFERENCE	14671302			
AUTHORS	2 (bases 1 to 1448)			
TITLE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,			
JOURNAL	Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,			
PUBMED	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,			
REFERENCE	Adams,M.D. and Cargill,M.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,			
PUBMED	Rockville, MD 20850, USA			
REFERENCE	This sequence was made by sequencing genomic exons and ordering			
AUTHORS	them based on alignment.			
TITLE	location/Qualifiers			
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PUBMED	/organism="Pan troglodytes"			
REFERENCE	/mol_type="genomic DNA"			
AUTHORS	/db_xref="taxon:9598"			
TITLE	<1...>.1448			
JOURNAL	/gene="PTGS1"			
PUBMED	/locus_tag="HCM5458"			
FEATURES				
SOURCE				
ORIGIN				
Query Match	19.4%; Score 657.2; DB 29; Length 1448;			
Best Local Similarity	66.8%; Pred.No.1e-111;			
Matches	932; Conservative 0; Mismatches 464; Indels 0; Gaps 0			
OY	414	GATCACAATTGATTGACAGTCCACCAACTTAATGCTGACATATGGCTACAAAGCTGGG	473	
D6	4	GCTCAACCTTATCCCAAGTCCGCCCATCAACTCACACATGATCACTTCACTGCTGGG	63	
OY	474	AAGCTTCTCTAAGCTCTCTCTATTATCTAGAGCCCTTCTCGTGTGCTGAATGTGCG	533	
D6	64	AGCTTTTCCCAAGTAGACTATTACATCGTATTTCTGCCCCCTGTGCTAAAGATTGCC	123	
OY	534	CGACTCCCTTGGGTGTCAAAGGTAAAAGCAGCTTCTGATTTCAATATGATTTGTGGAAA	593	
D6	124	CCACACCCATGGGGAACCAAGGGAAGAGACAGTTGCCAGATGCCGAGCTONNNNNCCGCC	183	
OY	594	AATTCCTTCTAGAGAAGATTCATCCCGATGCCAGGGCTCAACCATGATGTTTGAT	653	
D6	184	GCTTCTGTGTAGAGGAAGTTTCACTTCGACCCCACAGGACCAACTCATGTTTTGCT	243	
OY	654	TCTTTGCCAGCACTTTCACGACCAAGTTTTTCAAGACAGATCATAGCGAGGCGCACTT	713	
D6	244	TCTTTGGCAACAACCTTCAACCCACAGTTTCTTCAAAACCTTCTGGCAAGATGGGTCCTGGCT	303	

QY	714	TCACCAACGGGCTGGGCGCATGGGGGTGGACCTTAAATCATATATTACGGGTGAACCTCTGAGCA	773
Db	304	TCACCAAGGCTTGGGCGCATGGGGTGAACCTCGGCCACATTTATGGAGACATCTGGAGC	363
QY	774	GACAGCGTAAACTCGCGCTTTTCAAGAGTGAATAAATGAAATATCAATATGATGGAG	833
Db	364	GTGAGTATCAACTGCGGCTCTTTAAAGATGGAAACTCAAGTACCAAGTGTGGAGCGAG	423
QY	834	AGATGATTCCTCCACAGTTCAAAGATATCTCAGGCAGAGATGATCTACCCCTCCACAGTCC	893
Db	424	AAATGATCCGCTCGGTGAAGAAAGCGCTGTGTGATGACATACCCCGAGGCATCC	483
QY	894	CTGAGCATCTACGGTTTGTGTGGGGGCGAGAGGCTTTGGTCTGAGGCTGTGATGTA	953
Db	484	CGCCCCAGACCCAGATGGCTGTGGGCCAGAGAGGTGTTTGGGCTGTCTTCTGGGCTCATGC	543
QY	954	TGTATGCCACATCTGTGCTGTGGGGAACACAAACAGATATGTGATGTGCTTAAACAGAGC	1013
Db	544	TGTATGCCAGCTCTGGCTACGTGAGACAAACCGTGTGTGTACCTGTGTAAGAGCTGAGC	603
QY	1014	ATCTGTAATGGGGTGTAGTACAGATGTGTCACAGCAAGCAGGCTAAATCTGATAGAGAGA	1073
Db	604	ACCCCACTTGGGGGATGAGACAGCTTTTCCAGAGAACCGGCTCATCTCATAGGGGAGA	663
QY	1074	CTATTTAAGATTGTGATGGAAGATTATGTGCAACACTTGAAGTGTATCACTTAACCTGA	1133
Db	664	CCATCAGAGATTGTATGAGAGAGTACGTGACAGACGTAGTGTGCTATTTCTCGACGTGA	723
QY	1134	AATTTGACCCAGAACTATCTTTTCAACAAACAATTCCAGTACCAAAATGTGATTGTCTGT	1193
Db	724	AATTTGACCAAGAGCTGTCTGTGGGTGCCAGTTTCCAAATACCGAACCCGATTTGCCATGG	783
QY	1194	AATTTAACCCCTCTATCACTGAGATCCCTTGTGCTGACACCTTCAATTCAGTATGCC	1253
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QY	1254	AGAAATCAACTATCAACAGTTTATCTACAAACAACCTATATGTGCGGAACATGGAAATTA	1313
Db	844	AGAGTACAGTACGACACAGTCTTGTGTCAACACTCAATGTTGGTGAACATAGGGGCTCG	903
QY	1314	CCGAGTTGTGTAATCATTCACACAGGCAAAATGTGTGCAGGGTGTGCTGTGTGATGATG	1373
Db	904	AGGCGCTGTGTGATGCTTCTCTGTGCCAAGATGTGTGCCCGGATGGGTGGGGGACAGAAACA	963
QY	1374	TTCCACCCGCGATACAGAAAGTATCACAGGCTTTCATTTACACGAGCAGGACAGATGAAT	1433
Db	964	TGGACCAACATGTCTGTACGTGTGCTGTGATGTATCAAGGAATCTCGGAGAGTGGGCG	1023
QY	1434	ACCAAGCTTTTATAGAGTACCGGCAAAACGCTTTATGTGGAAGCCCTATGATCATTTGAAG	1493
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DEFINITION Mus musculus PTGS1 gene, VIRTUHL TRANSCRIPT, partial sequence,
AY415142 genomic survey sequence.
ACCESSION AY415142.1 GI:39771101
VERSION AY415142.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1448)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
2 (bases 1 to 1448)
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1448)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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/locus_tag="HcM5458"

ORIGIN

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Matches 924; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

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Db 4 GGTCAACCTTATCCCCAGCCCTCCGACCTACCAACTCAGCGCATGACTACATCAGCTGGG 63

474 AAGCCTTCTCTAACTCTCCTATTACTAGAGCCCTTCTCTGCTGCTGATATGGC 533
Db 64 AGTCTTCTCCATGTGAGCTACTATACCTGCAATTTGCTCTGTACCAAGACTGGC 123

534 CGATCTCCTTGGGTGTCAAAAGGTAAAGACAGCTTCTGATTTCAATGAGATGTGGAA 593
Db 124 CCACACCCATGGGGACCAAGAGGAAGAAACAGTTACAGATGTTCAGCTTGGCCCAAC 183

594 AATGCTTCTAGAGAAAGATTTATCTGATCTCCAGAGGCTCAACATGATGTTGCAT 653
Db 184 AGCTCTGTGTGAAGGAGGTTCATTTCTGCCCCCAGGGCACCAACATCTGTGTGCT 243

654 TCTTGGCCAGCACTTACGACAGATTTTTCAGAGCAGATCATTAAGAGAGGCCAGCTT 713
Db 244 TCTTGGCAACAACCTTACCCACAGCTTCTTAAGACCTCTGGAAGAGATGGGTCTGCT 303

714 TCACCAAGGGGTGGGCTCATGGGTGAGCTTAATCATATTACGATGAACTGTGCTGA 773
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